

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 81 to nucleotide 887;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yf9\_1 deposited under accession number ATCC 98861;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yf9\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yf9\_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;

- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 63 to nucleotide 305;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yh4\_1 deposited under accession number ATCC 98861;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh4\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
- (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yh4\_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 332 to nucleotide 685;

- (c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 422 to nucleotide 685;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yi4\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi4\_1 deposited under accession number ATCC 98861;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yi4\_1 deposited under accession number ATCC 98861;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yi4\_1 deposited under accession number ATCC 98861;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi4\_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:71;
- (b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 143 to nucleotide 502;
- (c) the nucleotide sequence of SEQ ID NO:71 from nucleotide 203 to nucleotide 502;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yj3\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj3\_1 deposited under accession number ATCC 98861;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yj3\_1 deposited under accession number ATCC 98861;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yj3\_1 deposited under accession number ATCC 98861;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yj3\_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins.



82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:73;
- (b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 30 to nucleotide 1004;
- (c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 1004;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yj7\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj7\_1 deposited under accession number ATCC 98861;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yj7\_1 deposited under accession number ATCC 98861;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yj7\_1 deposited under accession number ATCC 98861;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and

(c) the amino acid sequence encoded by the cDNA insert of clone yj7\_1 deposited under accession number ATCC 98861;  
the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 109 to nucleotide 1047;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yj10\_1 deposited under accession number ATCC 98861;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj10\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yj10\_1 deposited under accession number ATCC 98861;
- the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:77;
- (b) the nucleotide sequence of SEQ ID NO:77 from nucleotide 42 to nucleotide 1196;
- (c) the nucleotide sequence of SEQ ID NO:77 from nucleotide 558 to nucleotide 1196;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yj28\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj28\_1 deposited under accession number ATCC 98861;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yj28\_1 deposited under accession number ATCC 98861;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yj28\_1 deposited under accession number ATCC 98861;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:77.

87. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and

(c) the amino acid sequence encoded by the cDNA insert of clone yj28\_1 deposited under accession number ATCC 98861; the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 29 to nucleotide 1156;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 995 to nucleotide 1156;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yj29\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj29\_1 deposited under accession number ATCC 98861;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yj29\_1 deposited under accession number ATCC 98861;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yj29\_1 deposited under accession number ATCC 98861;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yj29\_1 deposited under accession number ATCC 98861;
- the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:81;
- (b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 93 to nucleotide 398;
- (c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 321 to nucleotide 398;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yj32\_1 deposited under accession number ATCC 98861;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj32\_1 deposited under accession number ATCC 98861;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yj32\_1 deposited under accession number ATCC 98861;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yj32\_1 deposited under accession number ATCC 98861;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yj32\_1 deposited under accession number ATCC 98861;

the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:83;
- (b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 167 to nucleotide 1264;
- (c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1264;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb186\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb186\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb186\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb186\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.

93. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yb186\_1 deposited under accession number ATCC 98872;
- the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:85;
- (b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 832 to nucleotide 1416;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb226\_1 deposited under accession number ATCC 98872;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb226\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
- (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb226\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:87;
- (b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 155 to nucleotide 745;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd50\_1 deposited under accession number ATCC 98872;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd50\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;



(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone yd50\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:89;

(b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 42 to nucleotide 317;

(c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 111 to nucleotide 317;

(d) the nucleotide sequence of the full-length protein coding sequence of clone yd51\_1 deposited under accession number ATCC 98872;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd51\_1 deposited under accession number ATCC 98872;

(f) the nucleotide sequence of a mature protein coding sequence of clone yd51\_1 deposited under accession number ATCC 98872;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd51\_1 deposited under accession number ATCC 98872;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.

99. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd51\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:91;
- (b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 7 to nucleotide 603;
- (c) the nucleotide sequence of SEQ ID NO:91 from nucleotide 244 to nucleotide 603;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd73\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd73\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd73\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd73\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:91.

101. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd73\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:93;
- (b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 367 to nucleotide 747;
- (c) the nucleotide sequence of SEQ ID NO:93 from nucleotide 667 to nucleotide 747;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ye43\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye43\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ye43\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ye43\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ye43\_1 deposited under accession number ATCC 98872;
- the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:95;
- (b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 632 to nucleotide 1492;
- (c) the nucleotide sequence of SEQ ID NO:95 from nucleotide 1460 to nucleotide 1492;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yh71\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh71\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yh71\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yh71\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone yh71\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:97;

(b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 349 to nucleotide 771;

(c) the nucleotide sequence of SEQ ID NO:97 from nucleotide 490 to nucleotide 771;

(d) the nucleotide sequence of the full-length protein coding sequence of clone yh100\_1 deposited under accession number ATCC 98872;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh100\_1 deposited under accession number ATCC 98872;

(f) the nucleotide sequence of a mature protein coding sequence of clone yh100\_1 deposited under accession number ATCC 98872;

- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yh100\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:97.

107. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yh100\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:99;
- (b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 165 to nucleotide 416;
- (c) the nucleotide sequence of SEQ ID NO:99 from nucleotide 261 to nucleotide 416;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yi3\_1 deposited under accession number ATCC 98872;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi3\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yi3\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yi3\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi3\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:101;
- (b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 141 to nucleotide 995;

- (c) the nucleotide sequence of SEQ ID NO:101 from nucleotide 213 to nucleotide 995;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yj23\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yj23\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yj23\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yj23\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:101.

111. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yj23\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:



- (a) the nucleotide sequence of SEQ ID NO:103;
- (b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 13 to nucleotide 747;
- (c) the nucleotide sequence of SEQ ID NO:103 from nucleotide 67 to nucleotide 747;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yl9\_1 deposited under accession number ATCC 98872;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yl9\_1 deposited under accession number ATCC 98872;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yl9\_1 deposited under accession number ATCC 98872;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yl9\_1 deposited under accession number ATCC 98872;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yl9\_1 deposited under accession number ATCC 98872;

the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:105;
- (b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 375 to nucleotide 728;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ya66\_1 deposited under accession number ATCC 98887;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya66\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:105.

115. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ya66\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:107;
- (b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 131 to nucleotide 457;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yb187\_1 deposited under accession number ATCC 98887;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb187\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:107.

117. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yb187\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:109;
- (b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 458 to nucleotide 676;

- (c) the nucleotide sequence of SEQ ID NO:109 from nucleotide 503 to nucleotide 676;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb219\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb219\_1 deposited under accession number ATCC 98887;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb219\_1 deposited under accession number ATCC 98887;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb219\_1 deposited under accession number ATCC 98887;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yb219\_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:111;
- (b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 238 to nucleotide 396;
- (c) the nucleotide sequence of SEQ ID NO:111 from nucleotide 277 to nucleotide 396;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb228\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb228\_1 deposited under accession number ATCC 98887;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb228\_1 deposited under accession number ATCC 98887;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb228\_1 deposited under accession number ATCC 98887;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yb228\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:113;
- (b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 6 to nucleotide 722;
- (c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 375 to nucleotide 722;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yc27\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc27\_1 deposited under accession number ATCC 98887;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yc27\_1 deposited under accession number ATCC 98887;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yc27\_1 deposited under accession number ATCC 98887;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.

123. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and

(c) the amino acid sequence encoded by the cDNA insert of clone yc27\_1 deposited under accession number ATCC 98887; the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:115;
- (b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 382 to nucleotide 681;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yc49\_1 deposited under accession number ATCC 98887;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yc49\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yc49\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:117;
- (b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 71 to nucleotide 364;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd40\_1 deposited under accession number ATCC 98887;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd40\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:117.

127. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;
- (b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd40\_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins.

128. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:



- (a) the nucleotide sequence of SEQ ID NO:119;
- (b) the nucleotide sequence of SEQ ID NO:119 from nucleotide 75 to nucleotide 725;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd64\_1 deposited under accession number ATCC 98887;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd64\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:119.

129. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:120;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd64\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

130. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:121;
- (b) the nucleotide sequence of SEQ ID NO:121 from nucleotide 256 to nucleotide 780;

- (c) the nucleotide sequence of SEQ ID NO:121 from nucleotide 412 to nucleotide 780;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ye47\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye47\_1 deposited under accession number ATCC 98887;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ye47\_1 deposited under accession number ATCC 98887;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ye47\_1 deposited under accession number ATCC 98887;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:122;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:121.

131. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:122;
- (b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye47\_1 deposited under accession number ATCC 98887;

the protein being substantially free from other mammalian proteins.

132. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:123;
- (b) the nucleotide sequence of SEQ ID NO:123 from nucleotide 127 to nucleotide 405;
- (c) the nucleotide sequence of SEQ ID NO:123 from nucleotide 268 to nucleotide 405;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yh50\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh50\_1 deposited under accession number ATCC 98887;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yh50\_1 deposited under accession number ATCC 98887;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yh50\_1 deposited under accession number ATCC 98887;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:124;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:123.

133. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:124;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yh50\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

134. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:125;
- (b) the nucleotide sequence of SEQ ID NO:125 from nucleotide 1175 to nucleotide 1480;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yh53\_1 deposited under accession number ATCC 98887;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh53\_1 deposited under accession number ATCC 98887;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:126;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:125.

135. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:126;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yh53\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

136. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:127;
  - (b) the nucleotide sequence of SEQ ID NO:127 from nucleotide 65 to nucleotide 319;
  - (c) the nucleotide sequence of SEQ ID NO:127 from nucleotide 173 to nucleotide 319;
  - (d) the nucleotide sequence of the full-length protein coding sequence of clone yh98\_1 deposited under accession number ATCC 98887;
  - (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh98\_1 deposited under accession number ATCC 98887;
  - (f) the nucleotide sequence of a mature protein coding sequence of clone yh98\_1 deposited under accession number ATCC 98887;
  - (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yh98\_1 deposited under accession number ATCC 98887;
  - (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:128;
  - (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;
  - (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
  - (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:127.
137. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:128;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yh98\_1 deposited under accession number ATCC 98887;
- the protein being substantially free from other mammalian proteins.

138. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:129;
- (b) the nucleotide sequence of SEQ ID NO:129 from nucleotide 122 to nucleotide 469;
- (c) the nucleotide sequence of SEQ ID NO:129 from nucleotide 263 to nucleotide 469;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ya69\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya69\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ya69\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya69\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:129.

139. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
- (b) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(c) the amino acid sequence encoded by the cDNA insert of clone ya69\_1 deposited under accession number ATCC 98915;  
the protein being substantially free from other mammalian proteins.

140. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:131;
- (b) the nucleotide sequence of SEQ ID NO:131 from nucleotide 36 to nucleotide 554;
- (c) the nucleotide sequence of SEQ ID NO:131 from nucleotide 183 to nucleotide 554;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd107\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd107\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd107\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd107\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:131.

141. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:132;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd107\_1 deposited under accession number ATCC 98915;
- the protein being substantially free from other mammalian proteins.

142. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:133;
- (b) the nucleotide sequence of SEQ ID NO:133 from nucleotide 8 to nucleotide 493;
- (c) the nucleotide sequence of SEQ ID NO:133 from nucleotide 53 to nucleotide 493;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd145\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd145\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd145\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd145\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:134;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:133.



143. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:134;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd145\_1 deposited under accession number ATCC 98915;
- the protein being substantially free from other mammalian proteins.

144. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:135;
- (b) the nucleotide sequence of SEQ ID NO:135 from nucleotide 21 to nucleotide 308;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yh24\_1 deposited under accession number ATCC 98915;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh24\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:136;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:135.

145. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:136;

- (b) a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yh24\_1 deposited under accession number ATCC 98915;
- the protein being substantially free from other mammalian proteins.

146. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:137;
- (b) the nucleotide sequence of SEQ ID NO:137 from nucleotide 214 to nucleotide 735;
- (c) the nucleotide sequence of SEQ ID NO:137 from nucleotide 634 to nucleotide 735;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yi11\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi11\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yi11\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yi11\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:138;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138, the fragment comprising eight contiguous amino acids of SEQ ID NO:138;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:137.

147. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:138;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:138, the fragment comprising eight contiguous amino acids of SEQ ID NO:138; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yi11\_1 deposited under accession number ATCC 98915;
- the protein being substantially free from other mammalian proteins.

148. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:139;
- (b) the nucleotide sequence of SEQ ID NO:139 from nucleotide 668 to nucleotide 937;
- (c) the nucleotide sequence of SEQ ID NO:139 from nucleotide 848 to nucleotide 937;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yi18\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi18\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yi18\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yi18\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:140;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:139.

149. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:140;
- (b) a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi18\_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins.

150. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:141;
- (b) the nucleotide sequence of SEQ ID NO:141 from nucleotide 171 to nucleotide 407;
- (c) the nucleotide sequence of SEQ ID NO:141 from nucleotide 258 to nucleotide 407;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk14\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk14\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk14\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk14\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:142;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142, the fragment comprising eight contiguous amino acids of SEQ ID NO:142;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:141.

151. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:142;
- (b) a fragment of the amino acid sequence of SEQ ID NO:142, the fragment comprising eight contiguous amino acids of SEQ ID NO:142; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk14\_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins.

152. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:143;
- (b) the nucleotide sequence of SEQ ID NO:143 from nucleotide 164 to nucleotide 457;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yk39\_1 deposited under accession number ATCC 98915;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk39\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:144;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144, the fragment comprising eight contiguous amino acids of SEQ ID NO:144;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:143.

153. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:144;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:144, the fragment comprising eight contiguous amino acids of SEQ ID NO:144; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk39\_1 deposited under accession number ATCC 98915;
- the protein being substantially free from other mammalian proteins.

154. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:145;
- (b) the nucleotide sequence of SEQ ID NO:145 from nucleotide 72 to nucleotide 500;
- (c) the nucleotide sequence of SEQ ID NO:145 from nucleotide 255 to nucleotide 500;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk91\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk91\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk91\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk91\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:146;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146, the fragment comprising eight contiguous amino acids of SEQ ID NO:146;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:145.

155. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:146;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:146, the fragment comprising eight contiguous amino acids of SEQ ID NO:146; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk91\_1 deposited under accession number ATCC 98915;
- the protein being substantially free from other mammalian proteins.

156. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:147;
- (b) the nucleotide sequence of SEQ ID NO:147 from nucleotide 174 to nucleotide 620;
- (c) the nucleotide sequence of SEQ ID NO:147 from nucleotide 240 to nucleotide 620;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk199\_1 deposited under accession number ATCC 98915;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk199\_1 deposited under accession number ATCC 98915;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk199\_1 deposited under accession number ATCC 98915;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk199\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:148;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:147.

157. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:148;

(b) a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk199\_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins.

158. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:149;

(b) the nucleotide sequence of SEQ ID NO:149 from nucleotide 325 to nucleotide 984;

(c) the nucleotide sequence of SEQ ID NO:149 from nucleotide 973 to nucleotide 984;

(d) the nucleotide sequence of the full-length protein coding sequence of clone y14\_1 deposited under accession number ATCC 98915;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone y14\_1 deposited under accession number ATCC 98915;

(f) the nucleotide sequence of a mature protein coding sequence of clone y14\_1 deposited under accession number ATCC 98915;



- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yl4\_1 deposited under accession number ATCC 98915;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:150;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150, the fragment comprising eight contiguous amino acids of SEQ ID NO:150;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:149.

159. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:150;
- (b) a fragment of the amino acid sequence of SEQ ID NO:150, the fragment comprising eight contiguous amino acids of SEQ ID NO:150; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yl4\_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins.

160. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:151;
- (b) the nucleotide sequence of SEQ ID NO:151 from nucleotide 119 to nucleotide 415;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yl14\_1 deposited under accession number ATCC 98915;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yl14\_1 deposited under accession number ATCC 98915;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:152;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:151.

161. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:152;

(b) a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152; and

(c) the amino acid sequence encoded by the cDNA insert of clone yl14\_1 deposited under accession number ATCC 98915;

the protein being substantially free from other mammalian proteins.

162. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:153;

(b) the nucleotide sequence of SEQ ID NO:153 from nucleotide 96 to nucleotide 377;

(c) the nucleotide sequence of SEQ ID NO:153 from nucleotide 225 to nucleotide 377;

(d) the nucleotide sequence of the full-length protein coding sequence of clone ya80\_1 deposited under accession number ATCC 98925;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ya80\_1 deposited under accession number ATCC 98925;

- (f) the nucleotide sequence of a mature protein coding sequence of clone ya80\_1 deposited under accession number ATCC 98925;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ya80\_1 deposited under accession number ATCC 98925;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:154;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154, the fragment comprising eight contiguous amino acids of SEQ ID NO:154;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:153.

163. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:154;
- (b) a fragment of the amino acid sequence of SEQ ID NO:154, the fragment comprising eight contiguous amino acids of SEQ ID NO:154; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ya80\_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins.

164. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:155;
- (b) the nucleotide sequence of SEQ ID NO:155 from nucleotide 118 to nucleotide 681;
- (c) the nucleotide sequence of SEQ ID NO:155 from nucleotide 622 to nucleotide 681;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd61\_1 deposited under accession number ATCC 98925;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd61\_1 deposited under accession number ATCC 98925;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd61\_1 deposited under accession number ATCC 98925;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd61\_1 deposited under accession number ATCC 98925;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:156;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:155.

165. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:156;
- (b) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd61\_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins.

166. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:157;

- (b) the nucleotide sequence of SEQ ID NO:157 from nucleotide 261 to nucleotide 614;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd88\_1 deposited under accession number ATCC 98925;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd88\_1 deposited under accession number ATCC 98925;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:158;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:157.

167. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:158;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd88\_1 deposited under accession number ATCC 98925;
- the protein being substantially free from other mammalian proteins.

168. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:159;
- (b) the nucleotide sequence of SEQ ID NO:159 from nucleotide 26 to nucleotide 475;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd109\_1 deposited under accession number ATCC 98925;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd109\_1 deposited under accession number ATCC 98925;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:160;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160, the fragment comprising eight contiguous amino acids of SEQ ID NO:160;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:159.

169. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:160;
- (b) a fragment of the amino acid sequence of SEQ ID NO:160, the fragment comprising eight contiguous amino acids of SEQ ID NO:160; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd109\_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins.

170. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:161;
- (b) the nucleotide sequence of SEQ ID NO:161 from nucleotide 79 to nucleotide 474;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd141\_1 deposited under accession number ATCC 98925;

- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd141\_1 deposited under accession number ATCC 98925;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:162;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:162, the fragment comprising eight contiguous amino acids of SEQ ID NO:162;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:161.

171. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:162;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:162, the fragment comprising eight contiguous amino acids of SEQ ID NO:162; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd141\_1 deposited under accession number ATCC 98925;
- the protein being substantially free from other mammalian proteins.

172. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:163;
- (b) the nucleotide sequence of SEQ ID NO:163 from nucleotide 45 to nucleotide 347;
- (c) the nucleotide sequence of SEQ ID NO:163 from nucleotide 135 to nucleotide 347;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd153\_1 deposited under accession number ATCC 98925;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd153\_1 deposited under accession number ATCC 98925;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd153\_1 deposited under accession number ATCC 98925;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd153\_1 deposited under accession number ATCC 98925;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:164;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:164, the fragment comprising eight contiguous amino acids of SEQ ID NO:164;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:163.

173. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:164;
- (b) a fragment of the amino acid sequence of SEQ ID NO:164, the fragment comprising eight contiguous amino acids of SEQ ID NO:164; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd153\_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins.

174. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:165;
- (b) the nucleotide sequence of SEQ ID NO:165 from nucleotide 114 to nucleotide 470;



- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd165\_1 deposited under accession number ATCC 98925;
  - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd165\_1 deposited under accession number ATCC 98925;
  - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:166;
  - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:166, the fragment comprising eight contiguous amino acids of SEQ ID NO:166;
  - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
  - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:165.
175. A protein comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:166;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:166, the fragment comprising eight contiguous amino acids of SEQ ID NO:166; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd165\_1 deposited under accession number ATCC 98925;
- the protein being substantially free from other mammalian proteins.
176. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence of SEQ ID NO:167;
  - (b) the nucleotide sequence of SEQ ID NO:167 from nucleotide 82 to nucleotide 663;
  - (c) the nucleotide sequence of SEQ ID NO:167 from nucleotide 139 to nucleotide 663;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd178\_1 deposited under accession number ATCC 98925;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd178\_1 deposited under accession number ATCC 98925;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd178\_1 deposited under accession number ATCC 98925;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd178\_1 deposited under accession number ATCC 98925;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:168;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:167.

177. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:168;
- (b) a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd178\_1 deposited under accession number ATCC 98925;

the protein being substantially free from other mammalian proteins.

178. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:169;

- (b) the nucleotide sequence of SEQ ID NO:169 from nucleotide 121 to nucleotide 450;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yd191\_1 deposited under accession number ATCC 98925;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd191\_1 deposited under accession number ATCC 98925;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:170;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:169.

179. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:170;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd191\_1 deposited under accession number ATCC 98925;
- the protein being substantially free from other mammalian proteins.

180. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:171;
- (b) the nucleotide sequence of SEQ ID NO:171 from nucleotide 33 to nucleotide 494;

- (c) the nucleotide sequence of the full-length protein coding sequence of clone ye7\_1 deposited under accession number ATCC 98924;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ye7\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:172;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172, the fragment comprising eight contiguous amino acids of SEQ ID NO:172;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:171.

181. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:172;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:172, the fragment comprising eight contiguous amino acids of SEQ ID NO:172; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ye7\_1 deposited under accession number ATCC 98924;
- the protein being substantially free from other mammalian proteins.

182. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:173;
- (b) the nucleotide sequence of SEQ ID NO:173 from nucleotide 1251 to nucleotide 1625;
- (c) the nucleotide sequence of SEQ ID NO:173 from nucleotide 1395 to nucleotide 1625;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone yf33\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yf33\_1 deposited under accession number ATCC 98924;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yf33\_1 deposited under accession number ATCC 98924;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yf33\_1 deposited under accession number ATCC 98924;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:174;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174, the fragment comprising eight contiguous amino acids of SEQ ID NO:174;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:173.

183. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:174;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:174, the fragment comprising eight contiguous amino acids of SEQ ID NO:174; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yf33\_1 deposited under accession number ATCC 98924;
- the protein being substantially free from other mammalian proteins.

184. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:175;

- (b) the nucleotide sequence of SEQ ID NO:175 from nucleotide 1299 to nucleotide 1640;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yi15\_1 deposited under accession number ATCC 98924;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi15\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:176;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:175.

185. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:176;
- (b) a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi15\_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins.

186. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:177;
- (b) the nucleotide sequence of SEQ ID NO:177 from nucleotide 85 to nucleotide 1377;

- (c) the nucleotide sequence of SEQ ID NO:177 from nucleotide 139 to nucleotide 1377;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yi17\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi17\_1 deposited under accession number ATCC 98924;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yi17\_1 deposited under accession number ATCC 98924;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yi17\_1 deposited under accession number ATCC 98924;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:178;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:177.

187. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:178;
- (b) a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yi17\_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins.

188. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:179;
- (b) the nucleotide sequence of SEQ ID NO:179 from nucleotide 50 to nucleotide 1075;
- (c) the nucleotide sequence of SEQ ID NO:179 from nucleotide 215 to nucleotide 1075;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk38\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk38\_1 deposited under accession number ATCC 98924;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk38\_1 deposited under accession number ATCC 98924;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk38\_1 deposited under accession number ATCC 98924;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:180;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180, the fragment comprising eight contiguous amino acids of SEQ ID NO:180;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:179.

189. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:180;
- (b) a fragment of the amino acid sequence of SEQ ID NO:180, the fragment comprising eight contiguous amino acids of SEQ ID NO:180; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk38\_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins.



190. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:181;
- (b) the nucleotide sequence of SEQ ID NO:181 from nucleotide 76 to nucleotide 348;
- (c) the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 348;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk51\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk51\_1 deposited under accession number ATCC 98924;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk51\_1 deposited under accession number ATCC 98924;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk51\_1 deposited under accession number ATCC 98924;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:182;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:181.

191. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:182;
- (b) a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk51\_1 deposited under accession number ATCC 98924;  
the protein being substantially free from other mammalian proteins.

192. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:183;
- (b) the nucleotide sequence of SEQ ID NO:183 from nucleotide 203 to nucleotide 577;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yk74\_1 deposited under accession number ATCC 98924;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk74\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:184;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:183.

193. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:184;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk74\_1 deposited under accession number ATCC 98924;
- the protein being substantially free from other mammalian proteins.

194. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:185;
- (b) the nucleotide sequence of SEQ ID NO:185 from nucleotide 38 to nucleotide 2170;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yk89\_1 deposited under accession number ATCC 98924;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk89\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:186;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:185.

195. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:186;
- (b) a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk89\_1 deposited under accession number ATCC 98924;

the protein being substantially free from other mammalian proteins.

196. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:187;
- (b) the nucleotide sequence of SEQ ID NO:187 from nucleotide 14 to nucleotide 742;
- (c) the nucleotide sequence of SEQ ID NO:187 from nucleotide 89 to nucleotide 742;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yl18\_1 deposited under accession number ATCC 98924;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yl18\_1 deposited under accession number ATCC 98924;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yl18\_1 deposited under accession number ATCC 98924;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yl18\_1 deposited under accession number ATCC 98924;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:188;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188, the fragment comprising eight contiguous amino acids of SEQ ID NO:188;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:187.

197. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:188;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:188, the fragment comprising eight contiguous amino acids of SEQ ID NO:188; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yl18\_1 deposited under accession number ATCC 98924;
- the protein being substantially free from other mammalian proteins.

198. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:189;
- (b) the nucleotide sequence of SEQ ID NO:189 from nucleotide 280 to nucleotide 615;
- (c) the nucleotide sequence of SEQ ID NO:189 from nucleotide 325 to nucleotide 615;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yb325\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yb325\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yb325\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yb325\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:190;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190, the fragment comprising eight contiguous amino acids of SEQ ID NO:190;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:189.

199. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:190;
- (b) a fragment of the amino acid sequence of SEQ ID NO:190, the fragment comprising eight contiguous amino acids of SEQ ID NO:190; and

(c) the amino acid sequence encoded by the cDNA insert of clone yb325\_1 deposited under accession number ATCC 98958; the protein being substantially free from other mammalian proteins.

200. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:191;
- (b) the nucleotide sequence of SEQ ID NO:191 from nucleotide 163 to nucleotide 429;
- (c) the nucleotide sequence of SEQ ID NO:191 from nucleotide 274 to nucleotide 429;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yd261\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yd261\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yd261\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yd261\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:192;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192, the fragment comprising eight contiguous amino acids of SEQ ID NO:192;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:191.

201. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:192;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:192, the fragment comprising eight contiguous amino acids of SEQ ID NO:192; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yd261\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

202. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:193;
- (b) the nucleotide sequence of SEQ ID NO:193 from nucleotide 1262 to nucleotide 1858;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yh33\_1 deposited under accession number ATCC 98958;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yh33\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:194;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:194, the fragment comprising eight contiguous amino acids of SEQ ID NO:194;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:193.

203. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:194;
- (b) a fragment of the amino acid sequence of SEQ ID NO:194, the fragment comprising eight contiguous amino acids of SEQ ID NO:194; and

(c) the amino acid sequence encoded by the cDNA insert of clone yh33\_1 deposited under accession number ATCC 98958; the protein being substantially free from other mammalian proteins.

204. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:195;
- (b) the nucleotide sequence of SEQ ID NO:195 from nucleotide 25 to nucleotide 1851;
- (c) the nucleotide sequence of SEQ ID NO:195 from nucleotide 250 to nucleotide 1851;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yi16\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yi16\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yi16\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yi16\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:196;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:196, the fragment comprising eight contiguous amino acids of SEQ ID NO:196;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:195.

205. A protein comprising an amino acid sequence selected from the group consisting of:



- (a) the amino acid sequence of SEQ ID NO:196;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:196, the fragment comprising eight contiguous amino acids of SEQ ID NO:196; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone y16\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

206. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:197;
- (b) the nucleotide sequence of SEQ ID NO:197 from nucleotide 739 to nucleotide 996;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yk46\_1 deposited under accession number ATCC 98958;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk46\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:198;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:198, the fragment comprising eight contiguous amino acids of SEQ ID NO:198;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:197.

207. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:198;
- (b) a fragment of the amino acid sequence of SEQ ID NO:198, the fragment comprising eight contiguous amino acids of SEQ ID NO:198; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk46\_1 deposited under accession number ATCC 98958; the protein being substantially free from other mammalian proteins.

208. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:199;
- (b) the nucleotide sequence of SEQ ID NO:199 from nucleotide 222 to nucleotide 605;
- (c) the nucleotide sequence of SEQ ID NO:199 from nucleotide 366 to nucleotide 605;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk84\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk84\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk84\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk84\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:200;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:200, the fragment comprising eight contiguous amino acids of SEQ ID NO:200;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:199.

209. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:200;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:200, the fragment comprising eight contiguous amino acids of SEQ ID NO:200; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk84\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

210. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:201;
- (b) the nucleotide sequence of SEQ ID NO:201 from nucleotide 140 to nucleotide 1036;
- (c) the nucleotide sequence of SEQ ID NO:201 from nucleotide 269 to nucleotide 1036;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk143\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk143\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk143\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk143\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:202;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:202, the fragment comprising eight contiguous amino acids of SEQ ID NO:202;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:201.

211. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:202;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:202, the fragment comprising eight contiguous amino acids of SEQ ID NO:202; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk143\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

212. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:203;
- (b) the nucleotide sequence of SEQ ID NO:203 from nucleotide 304 to nucleotide 636;
- (c) the nucleotide sequence of SEQ ID NO:203 from nucleotide 415 to nucleotide 636;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk156\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk156\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk156\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk156\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:204;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:204, the fragment comprising eight contiguous amino acids of SEQ ID NO:204;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:203.

213. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:204;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:204, the fragment comprising eight contiguous amino acids of SEQ ID NO:204; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk156\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

214. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:205;
- (b) the nucleotide sequence of SEQ ID NO:205 from nucleotide 571 to nucleotide 891;
- (c) the nucleotide sequence of SEQ ID NO:205 from nucleotide 745 to nucleotide 891;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk204\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk204\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk204\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk204\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:206;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:206, the fragment comprising eight contiguous amino acids of SEQ ID NO:206;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:205.

215. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:206;
- (b) a fragment of the amino acid sequence of SEQ ID NO:206, the fragment comprising eight contiguous amino acids of SEQ ID NO:206; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk204\_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins.

216. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:207;
- (b) the nucleotide sequence of SEQ ID NO:207 from nucleotide 283 to nucleotide 1560;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone yk224\_1 deposited under accession number ATCC 98958;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk224\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:208;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:208, the fragment comprising eight contiguous amino acids of SEQ ID NO:208;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:207.

217. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:208;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:208, the fragment comprising eight contiguous amino acids of SEQ ID NO:208; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone yk224\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

218. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:209;
- (b) the nucleotide sequence of SEQ ID NO:209 from nucleotide 485 to nucleotide 1465;
- (c) the nucleotide sequence of SEQ ID NO:209 from nucleotide 560 to nucleotide 1465;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone yk261\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone yk261\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone yk261\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone yk261\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:210;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:210, the fragment comprising eight contiguous amino acids of SEQ ID NO:210;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:209.

219. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:210;

(b) a fragment of the amino acid sequence of SEQ ID NO:210, the fragment comprising eight contiguous amino acids of SEQ ID NO:210; and

(c) the amino acid sequence encoded by the cDNA insert of clone yk261\_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins.

220. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:211;

(b) the nucleotide sequence of SEQ ID NO:211 from nucleotide 96 to nucleotide 821;

(c) the nucleotide sequence of the full-length protein coding sequence of clone ys3\_1 deposited under accession number ATCC 98958;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ys3\_1 deposited under accession number ATCC 98958;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:212;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:212, the fragment comprising eight contiguous amino acids of SEQ ID NO:212;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and



(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:211.

221. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:212;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:212, the fragment comprising eight contiguous amino acids of SEQ ID NO:212; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ys3\_1 deposited under accession number ATCC 98958;
- the protein being substantially free from other mammalian proteins.

222. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:213;
- (b) the nucleotide sequence of SEQ ID NO:213 from nucleotide 191 to nucleotide 499;
- (c) the nucleotide sequence of SEQ ID NO:213 from nucleotide 317 to nucleotide 499;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ys10\_1 deposited under accession number ATCC 98958;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ys10\_1 deposited under accession number ATCC 98958;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ys10\_1 deposited under accession number ATCC 98958;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ys10\_1 deposited under accession number ATCC 98958;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:214;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:214, the fragment comprising eight contiguous amino acids of SEQ ID NO:214;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:213.

223. A protein comprising an amino acid sequence selected from the group consisting of:

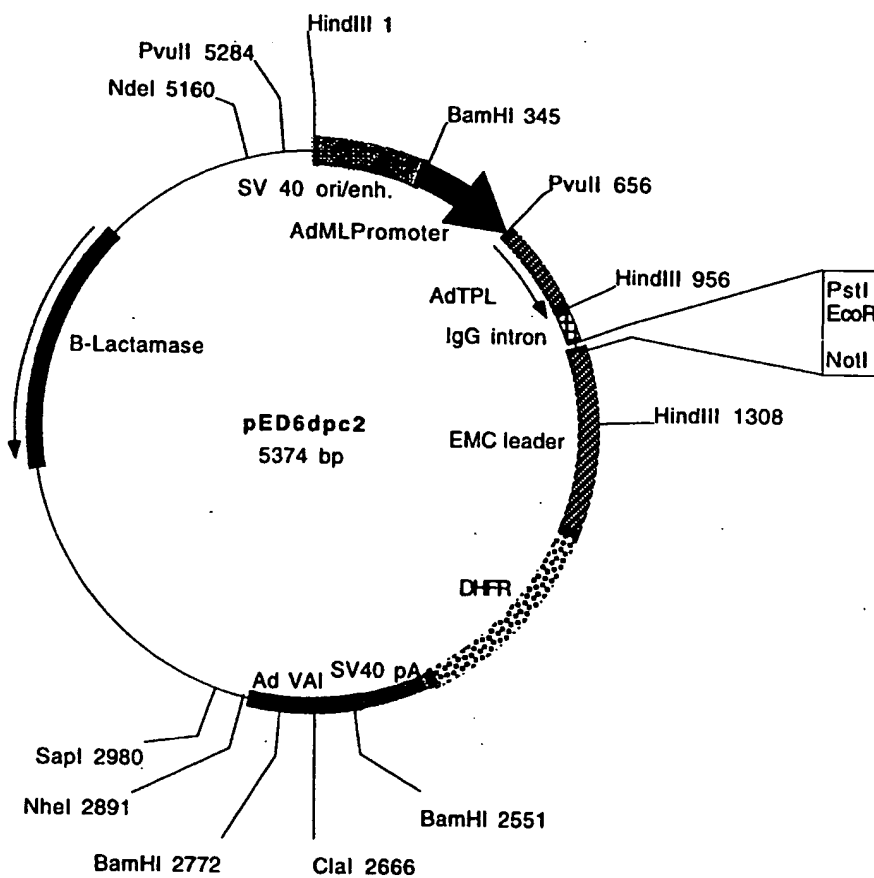
(a) the amino acid sequence of SEQ ID NO:214;

(b) a fragment of the amino acid sequence of SEQ ID NO:214, the fragment comprising eight contiguous amino acids of SEQ ID NO:214; and

(c) the amino acid sequence encoded by the cDNA insert of clone ys10\_1 deposited under accession number ATCC 98958;

the protein being substantially free from other mammalian proteins.

FIGURE 1A

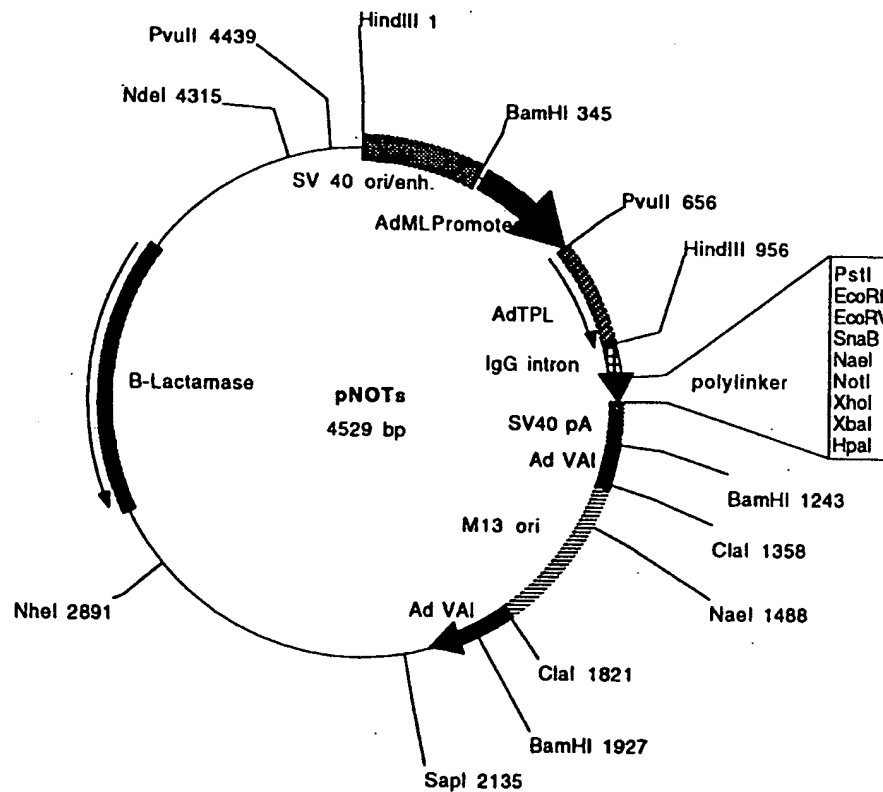


**Plasmid name:** pED6dpc2

**Plasmid size:** 5374 bp

**Comments/References:** pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



**Plasmid name:** pNOTs

**Plasmid size:** 4529 bp

**Comments/References:** pNOTs is a derivative of pMT2 (Kaufman et al, 1989. Mol. Cell. Biol. 9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the ClaI site. SST cDNAs are cloned between EcoRI and NotI

## SEQUENCE LISTING

<110> Wong, Gordon G.  
Clark, Hilary  
Fechtel, Kim  
Agostino, Michael J.  
Genetics Institute, Inc.

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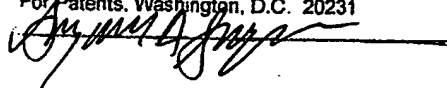
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Date of Deposit May 14, 1999

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&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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&lt;210&gt; 4

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (42)

&lt;400&gt; 4

Met Ile Val Leu Ser Leu Phe Ser Cys Pro Lys Leu Ile Gln Gly His  
 1 5 10 15

Arg Ser Met Asn Leu Ile Lys Thr Glu Met Gly Ile Ile Ala Gln Lys  
 20 25 30

Trp Glu Ile Thr Asn Phe Lys Ser Val Xaa Leu Ala Ser Tyr  
 35 40 45

&lt;210&gt; 5

&lt;211&gt; 4529

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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Met Ile Ser Met Ile Lys Met Phe Arg Glu Arg Asn Ile Leu Arg Asp
  1             5             10            15

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Asn Trp Ser Lys Thr His Leu Asp Phe Tyr Val Pro Lys Pro Leu Val
      20             25            30

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Trp Ser Gly Leu Ala Pro Ala Leu Ser Thr Ile Cys Leu Thr Val His
      35             40            45

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Ala Ser Cys Leu Cys Leu Pro Leu Glu Thr Met Arg Ala Glu Ile Arg
      50             55            60

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Pro Met Tyr Val Ala His Cys Cys Pro Gln Tyr Leu Ala Gln His Leu
      65             70            75            80

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Ala Pro Val Arg Thr Ser Tyr Ile Phe Pro Gly Leu Arg Gln Val Ser
      85             90            95

```

Pro Leu

&lt;210&gt; 7

&lt;211&gt; 3537

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

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&lt;210&gt; 8

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met Ile Met Ala Phe Ser Val Asn Lys Ala Asn Cys Asn Glu Ile Val  
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Leu Ala Ser Thr His Asp Val Gln Leu Asp Val Thr Ser Leu Leu  
20 25 30

Ala Cys Gln Ser Tyr Ile Trp Ile Gly Glu Glu Tyr Asp Arg Glu Ser  
35 40 45

Lys Ser Ser Asp Asp Val Asp Tyr Arg Gly Ser Thr Thr Thr Leu Tyr  
50 55 60

Gln Pro Ser Ala Thr Ser Tyr Ser Ala Ser Gln Val His Pro Pro Ser  
 65 70 75 80  
 Ser Leu Pro Trp Leu Gly Thr Gly Gln Thr Ser Thr Gly Ala Ser Val  
 85 90 95  
 Leu Met Lys Arg Asn Leu His Asn Val Lys Arg Met Thr Ser His Pro  
 100 105 110  
 Val His Gln Tyr Tyr Leu Thr Gly Ala Gln Asp Gly Ser Val Arg Met  
 115 120 125  
 Phe Glu Trp Thr Arg Pro Gln Gln Leu Val Cys Phe Arg Gln Ala Gly  
 130 135 140  
 Asn Ala Arg Val Thr Arg Leu Tyr Phe Asn Ser Gln Gly Asn Lys Cys  
 145 150 155 160  
 Gly Val Ala Asp Gly Glu Gly Phe Leu Ser Ile Trp Gln Val Asn Gln  
 165 170 175  
 Thr Ala Ser Asn Pro Lys Pro Tyr Met Ser Trp Gln Cys His Ser Lys  
 180 185 190  
 Ala Thr Ser Asp Phe Ala Phe Ile Thr Ser Ser Ser Leu Val Ala Thr  
 195 200 205  
 Ser Gly His Ser Asn Asp Asn Arg Asn Val Cys Leu Trp Asp Thr Leu  
 210 215 220  
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 Gly Ala Thr Val Leu Gln Tyr Ala Pro Lys Gln Gln Leu Leu Ile Ser  
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 Gly Gly Arg Lys Gly His Val Cys Ile Phe Asp Ile Arg Gln Arg Gln  
 260 265 270  
 Leu Ile His Thr Phe Gln Ala His Asp Ser Ala Ile Lys Ala Leu Ala  
 275 280 285  
 Leu Asp Pro Tyr Glu Glu Tyr Phe Thr Thr Gly Ser Ala Glu Gly Asn  
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 Ile Lys Val Trp Arg Leu Thr Gly His Gly Leu Ile His Ser Phe Lys  
 305 310 315 320  
 Ser Glu His Ala Lys Gln Ser Ile Phe Arg Asn Ile Gly Ala Gly Val  
 325 330 335  
 Met Gln Ile Asp Ile Ile Gln Gly Asn Arg Leu Phe Ser Cys Gly Ala  
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 Asp Gly Thr Leu Lys Thr Arg Val Leu Pro Asn Ala Phe Asn Ile Pro  
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 <211> 1466  
 <212> DNA  
 <213> Homo sapiens

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 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (25)

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 Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu Leu  
 35 40 45  
 Gln Ala Arg Gly Ile Thr Cys Ile Val Asn Ala Thr Ile Glu Ile Pro  
 50 55 60  
 Asn Phe Asn Trp Pro Gln Phe Glu Tyr Val Lys Val Pro Leu Ala Asp  
 65 70 75 80  
 Met Pro His Ala Pro Ile Gly Leu Tyr Phe Asp Thr Val Ala Asp Lys  
 85 90 95

Ile His Ser Val Ser Arg Lys His Gly Ala Thr Leu Val His Cys Ala  
 100 105 110

Ala Gly Val Ser Arg Ser Ala Thr Leu Cys Ile Ala Tyr Leu Met Lys  
 115 120 125

Phe His Asn Val Cys Leu Leu Glu Ala Tyr Asn Trp Val Lys Ala Arg  
 130 135 140

Arg Pro Val Ile Arg Pro Asn Val Gly Phe Trp Arg Gln Leu Ile Asp  
 145 150 155 160

Tyr Glu Arg Gln Leu Phe Gly Lys Ser Thr Val Lys Met Val Gln Thr  
 165 170 175

Pro Tyr Gly Ile Val Pro Asp Val Tyr Glu Lys Glu Ser Arg His Leu  
 180 185 190

Met Pro Tyr Trp Gly Ile  
 195

<210> 11  
 <211> 1521  
 <212> DNA  
 <213> Homo sapiens

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<210> 12  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (45)

&lt;400&gt; 12

Met Ala Val Ile Leu Leu Glu Ser Lys Gln Ser Val Val Trp Ser Arg  
 1 5 10 15

Val Cys Gly Phe Ser Gly Pro Ile Ile Met Ala Ala Ser Glu Ser Glu  
 20 25 30

Glu Ser His Arg Ala Val Gly Glu Leu Leu Leu Pro Xaa Pro Ser Pro  
 35 40 45

Phe Val Ala Pro Thr Leu Ala Ala Tyr Phe Cys Ser Ser Ala Gly Glu  
 50 55 60

Ser Val Trp Ala Ser Ser Ser Pro Ser Leu Ser Pro Cys Tyr Phe Met  
 65 70 75 80

Gly

&lt;210&gt; 13

&lt;211&gt; 697

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

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 aagcaagttt tttgggagag actagtgcac ctcagcaaac aagtttgga ctattatata 180  
 atcttgctcc agctgtgcaa atcatcttga ggatttcttt cttgatttta ttgggaatag 240  
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 tcacactcta caaactttac aagaagggt cacaatattt tgaggctttg ctagccaacc 360  
 cagaaggaag tggctctcga attcaagaca ataataatct ttctctgtcc ttgggtctgc 420  
 aagagaaaaa ttgaaaaaa ctttaagacag tggaaaacaa aatgaagaac ctagaaggga 480  
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 aaagatagag aacgctattg aaaaaaaaaa aaaaaaa 697

&lt;210&gt; 14

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Met Ser Thr Ser Ser Ser Ser Ser Trp Asp Asn Leu Leu Glu Ser Leu  
 1 5 10 15

Ser Leu Ser Thr Val Trp Asn Trp Ile Gln Ala Ser Phe Leu Gly Glu  
 20 25 30

Thr Ser Ala Pro Gln Gln Thr Ser Leu Gly Leu Leu Tyr Asn Leu Ala  
 35 40 45

Pro Ala Val Gln Ile Ile Leu Arg Ile Ser Phe Leu Ile Leu Leu Gly

50                      55                      60  
 Ile Gly Ile Tyr Ala Leu Trp Lys Arg Ser Ile Gln Ser Ile Gln Lys  
 65                      70                      75                      80  
 Thr Leu Leu Phe Val Ile Thr Leu Tyr Lys Leu Tyr Lys Lys Gly Ser  
                     85                      90                      95  
 His Ile Phe Glu Ala Leu Leu Ala Asn Pro Glu Gly Ser Gly Leu Arg  
                     100                      105                      110  
 Ile Gln Asp Asn Asn Asn Leu Phe Leu Ser Leu Gly Leu Gln Glu Lys  
                     115                      120                      125  
 Ile Leu Lys Lys Leu Lys Thr Val Glu Asn Lys Met Lys Asn Leu Glu  
                     130                      135                      140  
 Gly Ile Ile Val Ala Gln Lys Pro Ala Thr Lys Arg Asp Cys Ser Ser  
 145                      150                      155                      160  
 Glu Pro Tyr Cys Ser Cys Ser Asp Cys Gln Ser Pro Leu Ser Thr Ser  
                     165                      170                      175  
 Gly Phe Thr Ser Pro Ile  
                     180

<210> 15  
 <211> 983  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
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 agttacttag cttctctgtg ccccaactcc ctcatctgca cgcgagaatt gtaacagagc 180  
 cttcctcaga gcgatgatgg tgtttaggat gacatgcgct gcacagcaag tcctggccgt 240  
 ggcgggtgcc attgcagccc gtgggggtcac cctggaggcc gtgattgctg atgttgtgct 300  
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 ggcgtctctc tcgcctcaca ctgtgtgcac gggcagtgcg gacgggtgct ggcttggctc 420  
 ttccagccct gcctcgctcg gggcctgctg catcgtagct caggcctagg acccatctct 480  
 gtacctgcag gtcttgggtg ctgcccggca tgagtggagg agtttatcag aacaggacct 540  
 tttataggag gttttaactt tagaaggga tagaaaagtg tcatggcagc aatatttatt 600  
 tctagatcac cctgagtttt ttttctttgt ttkgtttwat tgcctcttt acaccatgag 660  
 tttttaatga tgaatgagtg aaggagtgc agtgccgggt gagcatccct tatccagatg 720  
 ctccagaatc ggaacacctc tgacaccgat gtggcacctc aggcattagct gagctagtga 780  
 cacctttgct ttctcatggg tcagtgtaca caaaccttgt ttcattgcaca aaattatcaa 840  
 aagtaccgca caaaattacc ctcaggctgt gtgtataagg tgtatatgaa acataaatga 900  
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 cgaatcagaa aaaaaaaaaa aaa 983

<210> 16  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Met Val Phe Arg Met Thr Cys Ala Ala Gln Gln Val Leu Ala Val  
                     1                      5                      10                      15

Ala Ala Ala Ile Ala Ala Arg Gly Val Thr Leu Glu Ala Val Ile Ala  
 20 25 30  
 Asp Val Val Leu Phe Leu Cys Leu Ala Leu Phe Phe Ser Val Pro Pro  
 35 40 45  
 Asp Ser Leu Cys Leu Arg Arg Thr Ala Ser Leu Ser Pro His Thr Val  
 50 55 60  
 Cys Thr Gly Ser Ala Asp Gly Cys Trp Leu Gly Leu Ser Ser Pro Ala  
 65 70 75 80  
 Ser Leu Gly Ala Cys Cys Ile Val Ala Gln Ala  
 85 90

<210> 17  
 <211> 267  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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 ccatcagtc cctgtttctc ttcctgagca gtttcttct gccactcagt caaaaggccc 180  
 acaaacatgt tcaccaagtc ctaacctcta gaaggagag agacttcaga gactgatttt 240  
 tagctgcaac caaaaaaaaa aaaaaaa 267

<210> 18  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Cys Met His Leu Gln Val Leu Gln Glu Pro Arg Val Leu His Ile  
 1 5 10 15  
 Leu Ser Phe Pro Gly Thr Phe Leu Ala Ala Arg Met Thr Glu Lys Ile  
 20 25 30  
 Ile Asn Leu Pro Ile Ser His Leu Phe Leu Phe Leu Ser Ser Phe Leu  
 35 40 45  
 Leu Pro Leu Ser Gln Lys Ala His Lys His Val His Gln Val Leu Thr  
 50 55 60  
 Ser Arg Arg Glu Arg Asp Phe Arg Asp  
 65 70

<210> 19  
 <211> 679  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
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 ggggttttcc agagtcagtc cccaattctg atgtttttat acgcaacact aggggtcctt 180  
 ctgaagttat cccggccctt gggaaactca cgtggcatgg ggcccccttc tgccctggtc 240

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tctttcatcc catctgtccc ggccccagag cctgtccagt ctggtcctct ctgtcctgct 300
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cagacgtgtc tgctagggac caccagctcc caagccgcat gacggtgctt tccttcaagg 420
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ggggcagctc tccctttttaa cttattggca gagctgggat gacttatagg tccctggctc 540
agtgagtaag caagttcaga gacttggtt tggccatttt gttctcttag gctcatcctt 600
ggatgccaac agggaaataa cctgccagat ttcagtcact actttttaga agttaaaaaa 660
aaaaaaaaaa aaaaaaaaaa

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<210> 20  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Cys Leu Gly Phe Leu Arg Gly Phe Pro Glu Ser Val Pro Asn Ser  
 1 5 10 15  
 Asp Val Phe Ile Arg Asn Thr Arg Gly Pro Ser Glu Val Ile Pro Ala  
 20 25 30  
 Pro Gly Lys Leu Thr Trp His Gly Ala Pro Phe Cys Pro Gly Leu Phe  
 35 40 45  
 His Pro Ile Cys Pro Gly Pro Arg Ala Cys Pro Val Trp Ser Ser Leu  
 50 55 60  
 Ser Cys Leu Val Cys His His Val Met Leu Gly Trp Leu Val Phe Ala  
 65 70 75 80  
 Ala Ser Leu Pro Lys Leu Thr Asp Val Ser Ala Arg Asp His Gln Leu  
 85 90 95  
 Pro Ser Arg Met Thr Val Leu Ser Phe Lys Val Gln Arg Leu Pro Phe  
 100 105 110  
 Gln Ser Gly Pro Ser Pro Thr Ser  
 115 120

<210> 21  
 <211> 3340  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 actgatctgc tctgaaaact atattactta caagaacttt ggtgaccagc cagatatccg 120  
 ctgtccaatt cccaggaggc ggaatgacct ggtgaccct gaaagaggaa tgatttttgt 180  
 ctgctctgca acccataaaa ccaaatcgat gttcttcttt ttggctcaaa ctgagcaggg 240  
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 tgaagaacct gaggtttcat cagccatgcc tctggaagaa ggagacacat tcttttttca 480  
 gccmagacca cttaaaaacc ttgtgctggt tgatgagttg gacagcctct ctcccattct 540  
 gttttgccag atagctgatc tggccaatga agatactcca cagttgtatg tggcctgtgg 600  
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 tgagtttgat gcctacatca ttgtgtcttt cgtgaatgcc accctagtgt tgtccattgg 780  
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&lt;210&gt; 22

&lt;211&gt; 933

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

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Met Ile Phe Val Cys Ser Ala Thr His Lys Thr Lys Ser Met Phe Phe
  1                      5                      10                      15

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Phe Leu Ala Gln Thr Glu Gln Gly Asp Ile Phe Lys Ile Thr Leu Glu
      20                      25                      30

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Thr Asp Glu Asp Met Val Thr Glu Ile Arg Leu Lys Tyr Phe Asp Thr
      35                      40                      45

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Val Pro Val Ala Ala Ala Met Cys Val Leu Lys Thr Gly Phe Leu Phe
      50                      55                      60

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Val Ala Ser Glu Phe Gly Asn His Tyr Leu Tyr Gln Ile Ala His Leu  
 65 70 75 80  
 Gly Asp Asp Asp Glu Glu Pro Glu Phe Ser Ser Ala Met Pro Leu Glu  
 85 90 95  
 Glu Gly Asp Thr Phe Phe Phe Gln Pro Arg Pro Leu Lys Asn Leu Val  
 100 105 110  
 Leu Val Asp Glu Leu Asp Ser Leu Ser Pro Ile Leu Phe Cys Gln Ile  
 115 120 125  
 Ala Asp Leu Ala Asn Glu Asp Thr Pro Gln Leu Tyr Val Ala Cys Gly  
 130 135 140  
 Arg Gly Pro Arg Ser Ser Leu Arg Val Leu Arg His Gly Leu Glu Val  
 145 150 155 160  
 Ser Glu Met Ala Val Ser Glu Leu Pro Gly Asn Pro Asn Ala Val Trp  
 165 170 175  
 Thr Val Arg Arg His Ile Glu Asp Glu Phe Asp Ala Tyr Ile Ile Val  
 180 185 190  
 Ser Phe Val Asn Ala Thr Leu Val Leu Ser Ile Gly Glu Thr Val Glu  
 195 200 205  
 Glu Val Thr Asp Ser Gly Phe Leu Gly Thr Thr Pro Thr Leu Ser Cys  
 210 215 220  
 Ser Leu Leu Gly Asp Asp Ala Leu Val Gln Val Tyr Pro Asp Gly Ile  
 225 230 235 240  
 Arg His Ile Arg Ala Asp Lys Arg Val Asn Glu Trp Lys Thr Pro Gly  
 245 250 255  
 Lys Lys Thr Ile Val Lys Cys Ala Val Asn Gln Arg Gln Val Val Ile  
 260 265 270  
 Ala Leu Thr Gly Gly Glu Leu Val Tyr Phe Glu Met Asp Pro Ser Gly  
 275 280 285  
 Gln Leu Asn Glu Tyr Thr Glu Arg Lys Glu Met Ser Ala Asp Val Val  
 290 295 300  
 Cys Met Ser Leu Ala Asn Val Pro Pro Gly Glu Gln Arg Ser Arg Phe  
 305 310 315 320  
 Leu Ala Val Gly Leu Val Asp Asn Thr Val Arg Ile Ile Ser Leu Asp  
 325 330 335  
 Pro Ser Asp Cys Leu Gln Pro Leu Ser Met Gln Ala Leu Pro Ala Gln  
 340 345 350  
 Pro Glu Ser Leu Cys Ile Val Glu Met Gly Gly Thr Glu Lys Gln Asp  
 355 360 365  
 Glu Leu Gly Glu Arg Gly Ser Ile Gly Phe Leu Tyr Leu Asn Ile Gly  
 370 375 380

Leu Gln Asn Gly Val Leu Leu Arg Thr Val Leu Asp Pro Val Thr Gly  
 385 390 395 400  
 Asp Leu Ser Asp Thr Arg Thr Arg Tyr Leu Gly Ser Arg Pro Val Lys  
 405 410 415  
 Leu Phe Arg Val Arg Met Gln Gly Gln Glu Ala Val Leu Ala Met Ser  
 420 425 430  
 Ser Arg Ser Trp Leu Ser Tyr Ser Tyr Gln Ser Arg Phe His Leu Thr  
 435 440 445  
 Pro Leu Ser Tyr Glu Thr Leu Glu Phe Ala Ser Gly Phe Ala Ser Glu  
 450 455 460  
 Gln Cys Pro Glu Gly Ile Val Ala Ile Ser Thr Asn Thr Leu Arg Ile  
 465 470 475 480  
 Leu Ala Leu Glu Lys Leu Gly Ala Val Phe Asn Gln Val Ala Phe Pro  
 485 490 495  
 Leu Gln Tyr Thr Pro Arg Lys Phe Val Ile His Pro Glu Ser Asn Asn  
 500 505 510  
 Leu Ile Ile Ile Glu Thr Asp His Asn Ala Tyr Thr Glu Ala Thr Lys  
 515 520 525  
 Ala Gln Arg Lys Gln Gln Met Ala Glu Glu Met Val Glu Ala Ala Gly  
 530 535 540  
 Glu Asp Glu Arg Glu Leu Ala Ala Glu Met Ala Ala Ala Phe Leu Asn  
 545 550 555 560  
 Glu Asn Leu Pro Glu Ser Ile Phe Gly Ala Pro Lys Ala Gly Asn Gly  
 565 570 575  
 Gln Trp Ala Ser Val Ile Arg Val Met Asn Pro Ile Gln Gly Asn Thr  
 580 585 590  
 Leu Asp Leu Val Gln Leu Glu Gln Asn Glu Ala Ala Phe Ser Val Ala  
 595 600 605  
 Val Cys Arg Phe Ser Asn Thr Gly Glu Asp Trp Tyr Val Leu Val Gly  
 610 615 620  
 Val Ala Lys Asp Leu Ile Leu Asn Pro Arg Ser Val Ala Gly Gly Phe  
 625 630 635 640  
 Val Tyr Thr Tyr Lys Leu Val Asn Asn Gly Glu Lys Leu Glu Phe Leu  
 645 650 655  
 His Lys Thr Pro Val Glu Glu Val Pro Ala Ala Ile Ala Pro Phe Gln  
 660 665 670  
 Gly Arg Val Leu Ile Gly Val Gly Lys Leu Leu Arg Val Tyr Asp Leu  
 675 680 685  
 Gly Lys Lys Lys Leu Leu Arg Lys Cys Glu Asn Lys His Ile Ala Asn  
 690 695 700

Tyr Ile Ser Gly Ile Gln Thr Ile Gly His Arg Val Ile Val Ser Asp  
 705 710 715 720  
 Val Gln Glu Ser Phe Ile Trp Val Arg Tyr Lys Arg Asn Glu Asn Gln  
 725 730 735  
 Leu Ile Ile Phe Ala Asp Asp Thr Tyr Pro Arg Trp Val Thr Thr Ala  
 740 745 750  
 Ser Leu Leu Asp Tyr Asp Thr Val Ala Gly Ala Asp Lys Phe Gly Asn  
 755 760 765  
 Ile Cys Val Val Arg Leu Pro Pro Asn Thr Asn Asp Glu Val Asp Glu  
 770 775 780  
 Asp Pro Thr Gly Asn Lys Ala Leu Trp Asp Arg Gly Leu Leu Asn Gly  
 785 790 795 800  
 Ala Ser Gln Lys Ala Glu Val Ile Met Asn Tyr His Val Gly Glu Thr  
 805 810 815  
 Val Leu Ser Leu Gln Lys Thr Thr Leu Ile Pro Gly Gly Ser Glu Ser  
 820 825 830  
 Leu Val Tyr Thr Thr Leu Ser Gly Gly Ile Gly Ile Leu Val Pro Phe  
 835 840 845  
 Thr Ser His Glu Asp His Asp Phe Phe Gln His Val Glu Met His Leu  
 850 855 860  
 Arg Ser Glu His Pro Pro Leu Cys Gly Arg Asp His Leu Ser Phe Arg  
 865 870 875 880  
 Ser Tyr Tyr Phe Pro Val Lys Asn Val Ile Asp Gly Asp Leu Cys Glu  
 885 890 895  
 Gln Phe Asn Ser Met Glu Pro Asn Lys Gln Lys Asn Val Ser Glu Glu  
 900 905 910  
 Leu Asp Arg Thr Pro Pro Glu Val Ser Lys Lys Leu Glu Asp Ile Arg  
 915 920 925  
 Thr Arg Tyr Ala Phe  
 930

&lt;210&gt; 23

&lt;211&gt; 1496

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

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&lt;210&gt; 24

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (12)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (15)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (84)

&lt;400&gt; 24

```

Met Glu Gly Leu Ala Pro Gly Ser Cys Gly Ser Xaa Gly Ser Xaa Thr
  1             5             10             15

Pro Gly Gly Gly Gly Gly Thr Ser Ala Pro Gln Pro His Pro Ala Leu
      20             25             30

Pro Ser Arg Ser Leu Gly Cys Lys Pro Val Ser Ser Val Val Ser Arg
      35             40             45

Pro Leu Leu Leu Cys Met Ile Arg Leu Gly Asn Leu Arg Ser Ala Met
      50             55             60

Leu Cys Ser Gly Ser Pro Cys Leu Pro Pro Arg Gly Ala Leu Leu Pro
      65             70             75             80

Leu Gly Leu Xaa Val Pro Gly Arg Gly Leu Cys Gly Ala Cys Asp Gly
      85             90             95

Ser Ser Trp Lys Thr Leu Trp Gly Arg Gly Glu Ala His Glu Ala Met
      100            105            110

Gly Thr Ala His His Gly Glu His Thr Cys Arg Trp Gly Gly Leu Pro
      115            120            125

```

Phe Pro Thr Ala Leu Arg Arg Cys Thr Trp Pro Gly Leu Met Ser Cys  
 130 135 140  
 Pro Glu Pro Pro Leu Gly Val Thr Glu Gly Arg Ala Gly Ser Thr Asp  
 145 150 155 160  
 Ala Pro Ala Arg Gly Leu Ser Gly Ala Ser Ala Asp Arg Leu Ser Ser  
 165 170 175  
 Arg Pro Leu Phe His Gly Gly Gly Pro Ser Ser Asp Asp Asp Ala Gly  
 180 185 190  
 Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln Asn Asp Lys Gly Lys  
 195 200 205  
 Asn Val Arg Gln Arg Asn Ser Ser  
 210 215

&lt;210&gt; 25

&lt;211&gt; 2113

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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<210> 26

<211> 315

<212> PRT

<213> Homo sapiens

<400> 26

Met Ala Ala Gly Val Pro Cys Ala Leu Val Thr Ser Cys Ser Ser Val  
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 20 25 30  
 Ile Val Glu Val Thr Ser Asn Asp Ala Val Arg Phe Tyr Pro Trp Thr  
 35 40 45  
 Ile Asp Asn Lys Tyr Tyr Ser Ala Asp Ile Asn Leu Cys Val Val Pro  
 50 55 60  
 Asn Lys Phe Leu Val Thr Ala Glu Ile Ala Glu Ser Val Gln Ala Phe  
 65 70 75 80  
 Val Val Tyr Phe Asp Ser Thr Gln Lys Ser Gly Leu Asp Ser Val Ser  
 85 90 95  
 Ser Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Glu Val Met Ile Leu  
 100 105 110  
 Val Cys Asp Arg Val Ser Glu Asp Gly Ile Asn Arg Gln Lys Ala Gln  
 115 120 125  
 Glu Trp Cys Leu Lys His Gly Phe Glu Leu Val Glu Leu Ser Pro Glu  
 130 135 140  
 Glu Leu Pro Glu Glu Asp Asp Asp Phe Pro Glu Ser Thr Gly Val Lys  
 145 150 155 160  
 Arg Ile Val Gln Ala Leu Asn Ala Asn Val Trp Ser Asn Val Val Met  
 165 170 175  
 Lys Asn Asp Arg Asn Gln Gly Phe Ser Leu Leu Asn Ser Leu Thr Gly  
 180 185 190  
 Thr Asn His Ser Ile Gly Ser Ala Asp Pro Cys His Pro Glu Gln Pro  
 195 200 205  
 His Leu Pro Ala Ala Asp Ser Thr Glu Ser Leu Ser Asp His Arg Gly  
 210 215 220  
 Gly Ala Ser Asn Thr Thr Asp Ala Gln Val Asp Ser Ile Val Asp Pro  
 225 230 235 240  
 Met Leu Asp Leu Asp Ile Gln Glu Leu Ala Ser Leu Thr Thr Gly Gly  
 245 250 255  
 Gly Asp Val Glu Asn Phe Glu Arg Leu Phe Ser Lys Leu Lys Glu Met  
 260 265 270

Lys Asp Lys Ala Ala Thr Leu Pro His Glu Gln Arg Lys Val His Ala  
 275 280 285

Glu Lys Val Ala Lys Ala Phe Trp Met Ala Ile Gly Gly Asp Arg Asp  
 290 295 300

Glu Ile Glu Gly Leu Ser Ser Asp Glu Glu His  
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<210> 27

<211> 1541

<212> DNA

<213> Homo sapiens

<400> 27

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<210> 28

<211> 309

<212> PRT

<213> Homo sapiens

<400> 28

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Asn Ile Cys Leu Ala Thr Lys Asp Arg Gln Asn Pro Ser Leu Val Trp  
 20 25 30

Leu Phe Thr Gly Met Phe Cys Ile Tyr Ser Leu Phe Phe Ala Trp Arg  
 35 40 45

Ala Asn Leu Asp Ile Ser Lys Pro Leu Phe Met Gly Val Val Glu Arg  
 50 55 60



Phe Trp Met Gln Ser Asn Ala Val Val Ala Val Leu Ala Gly Ile Gly  
 65 70 75 80  
 Leu Ala Ala Val Val Ser Glu Thr Asn Arg Val Leu Asn Ser Asn Gly  
 85 90 95  
 Leu Gln Cys Leu Glu Trp Leu Ser Ala Thr Leu Phe Val Val Tyr Gln  
 100 105 110  
 Ile Tyr Ser Asn Tyr Arg Lys Glu Thr Phe Val Cys Ile Gly Ile His  
 115 120 125  
 Glu Gly Asp Pro Thr Trp Lys Lys Asn Tyr Ser Leu Trp Pro Trp Gly  
 130 135 140  
 Ser Cys Asp Lys Leu Val Pro Leu Glu Ile Val Phe Asn Pro Glu Glu  
 145 150 155 160  
 Trp Ile Lys Leu Thr Lys Asn Ile Tyr Asn Trp Thr Glu Glu Tyr Gly  
 165 170 175  
 Arg Phe Asp Pro Ser Ser Trp Glu Ser Val Ala Asn Glu Glu Met Trp  
 180 185 190  
 Gln Ala Arg Met Lys Thr Pro Phe Phe Ile Phe Asn Leu Ala Glu Thr  
 195 200 205  
 Ala His Met Pro Ser Lys Val Lys Ala Gln Leu Tyr Ala Gln Ala Tyr  
 210 215 220  
 Asp Leu Tyr Lys Glu Ile Val Tyr Leu Gln Lys Glu His Pro Val Asn  
 225 230 235 240  
 Trp His Lys Asn Tyr Ala Ile Ala Cys Glu Arg Met Leu Arg Leu Gln  
 245 250 255  
 Ala Arg Asp Ala Asp Pro Glu Val Leu Leu Ser Glu Thr Ile Arg His  
 260 265 270  
 Phe Arg Leu Tyr Ser Gln Lys Ala Pro Asn Asp Pro Gln Gln Ala Asp  
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<210> 29  
 <211> 539  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (495)

<400> 29

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<210> 30

<211> 145

<212> PRT

<213> Homo sapiens

<400> 30

Met Gly Pro Glu Glu Lys Thr Ile Met Thr Asp Arg Ser Ala Ala Val  
 1 5 10 15

Phe Ile Gln Ala Trp Trp Arg Gly Met Leu Val Arg Arg His Cys Cys  
 20 25 30

Met Gln Pro Ser Gly Leu Gly Ser Phe Ser Ala Gly Gly Gly Arg Cys  
 35 40 45

Trp Arg Ser Cys Trp Gln Arg Gly Gly Gly Trp Cys Trp Ser Ser Met  
 50 55 60

Cys Ser Arg Asn Gly Gln Gln Ser Gly Cys Ser Pro Gly Ser Ala Cys  
 65 70 75 80

Gly Val Ser Ala Ser Val Thr Val Val Cys Ser Thr Leu Ser Ala Ser  
 85 90 95

Ser Arg Ser Ile Gly Ala Gly Thr Ala Ala Ile Pro Val Ala Lys Leu  
 100 105 110

Arg Ala Thr Met Asn Ser Lys Lys Thr Asn Lys Lys Asn Asn Met Lys  
 115 120 125

Thr Pro Trp Ala Asn Arg Leu Val Arg Cys Asn Asn Ala Tyr Pro Phe  
 130 135 140

His

145

<210> 31

<211> 2408

<212> DNA

<213> Homo sapiens

<400> 31

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 tccagcattg ttctgcttca cccttgactg cggtgtcttg cagtttctgt gtgctgccag 300  
 gatattatat ggaactggag aagttggagt caggtctctg aagctagagt ttcactaatt 360  
 agatgcctct gtacatgaga actattactg tctgcaggtc catatagcta agctgccagg 420

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aaaaaaaaa 2408

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&lt;210&gt; 32

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

```

Met Ser Leu Thr Pro Gln Gly Leu Ala Trp Ile Pro Lys Gln Leu Gln
  1             5             10             15

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Gln Ile Ser Ser Glu Pro Gly Thr Glu Asn Ser Val Leu Leu Leu
      20             25             30

```

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Arg Lys Glu Val Phe Arg Met Pro Arg Ala Glu Gln Pro Val Ile Thr
      35             40             45

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Leu Val Cys Ser His Leu Gly Ala His Pro His Asp Ala Val Ala Val
      50             55             60

```

```

Ala Pro Ser Cys Gln Val Leu Arg Glu Trp Glu Ile Leu Pro Pro His
      65             70             75             80

```

&lt;210&gt; 33

&lt;211&gt; 970

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

```

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```

&lt;210&gt; 34

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

```

Met Glu Ser Glu Trp Gly Cys Glu Arg Ser Ser Thr Ala Ser Ala Arg
 1             5             10            15

Ser Val Pro His Asn Gly Leu Leu Glu Phe Val Ser Arg Pro Val Gln
          20             25             30

Asp Cys Leu Leu Leu Gln Leu Ile Ser Phe Ile Ser Phe Pro Pro Pro
 35             40             45

Pro Thr Ser Thr Lys Ser Gly Glu Glu Trp Glu Arg Thr Gly Lys Leu
 50             55             60

Thr Gly Gln Arg Glu Lys Ala Asn Ser His Ser Ala Gly Gly Gly Thr
 65             70             75             80

Pro Gly Met Gln Tyr Pro Thr Val Ser Ser Leu Leu Ser Cys Asn Leu
          85             90             95

Gln Val Ile Val Phe Leu Ile Cys Ser Phe Phe Phe Phe Ser Ser Val
 100            105            110

Ala Gly Lys Gln Ser Asn Asp Gly
 115            120

```

&lt;210&gt; 35

&lt;211&gt; 2084

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

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&lt;210&gt; 36

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

```

Met Gly Arg Lys Lys Lys Lys Gln Leu Lys Pro Trp Cys Trp Tyr Cys
 1             5             10             15

His Arg Asp Phe Asp Asp Glu Lys Ile Leu Ile Gln His Gln Lys Ala
 20             25             30

Lys His Phe Lys Cys His Ile Cys His Lys Lys Leu Tyr Thr Gly Pro
 35             40             45

Gly Leu Ala Ile His Cys Met Gln Val His Lys Glu Thr Ile Asp Ala
 50             55             60

Val Pro Asn Ala Ile Pro Gly Arg Thr Asp Ile Glu Leu Glu Ile Tyr
 65             70             75             80

Gly Met Glu Gly Ile Pro Glu Lys Asp Met Asp Glu Arg Arg Arg Leu
 85             90             95

Leu Glu Gln Lys Thr Gln Glu Ser Leu Lys Lys Lys Gln Gln Asp Asp
100            105            110

```

Ser Asp Glu Tyr Asp Asp Asp Asp Ser Ala Ala Ser Thr Ser Phe Gln  
 115 120 125  
 Pro Gln Pro Val Gln Pro Gln Gln Gly Tyr Ile Pro Pro Met Ala Gln  
 130 135 140  
 Pro Gly Leu Pro Pro Val Pro Gly Ala Pro Gly Met Pro Pro Gly Ile  
 145 150 155 160  
 Pro Pro Leu Met Pro Arg Val Pro Pro Leu Met Pro Gly Met Pro Pro  
 165 170 175  
 Val Met Pro Gly Met Pro Pro Gly Leu His His Gln Arg Lys Tyr Thr  
 180 185 190  
 Gln Ser Phe Cys Gly Glu Asn Ile Met Met Pro Met Gly Gly Met Met  
 195 200 205  
 Pro Pro Gly Pro Gly Ile Pro Pro Leu Met Pro Gly Met Pro Pro Gly  
 210 215 220  
 Met Pro Pro Pro Val Pro Arg Pro Gly Ile Pro Pro Met Thr Gln Ala  
 225 230 235 240  
 Gln Ala Val Ser Ala Pro Gly Ile Leu Asn Arg Pro Pro Ala Pro Thr  
 245 250 255  
 Ala Thr Val Pro Ala Pro Gln Pro Pro Val Thr Lys Pro Leu Phe Pro  
 260 265 270  
 Ser Ala Gly Gln Ala Gln Ala Ala Val Gln Gly Pro Val Gly Thr Asp  
 275 280 285  
 Phe Lys Pro Leu Asn Ser Thr Pro Ala Thr Thr Thr Glu Pro Pro Lys  
 290 295 300  
 Pro Thr Phe Pro Ala Tyr Thr Gln Ser Thr Ala Ser Thr Thr Ser Thr  
 305 310 315 320  
 Thr Asn Ser Thr Ala Ala Lys Pro Ala Ala Ser Ile Thr Ser Lys Pro  
 325 330 335  
 Ala Thr Leu Thr Thr Thr Ser Ala Thr Ser Lys Leu Ile His Pro Asp  
 340 345 350  
 Glu Asp Ile Ser Leu Glu Glu Arg Arg Ala Gln Leu Pro Lys Tyr Gln  
 355 360 365  
 Arg Asn Leu Pro Arg Pro Gly Gln Ala Pro Ile Gly Asn Pro Pro Val  
 370 375 380  
 Gly Pro Ile Gly Gly Met Met Pro Pro Gln Pro Gly Ile Pro Gln Gln  
 385 390 395 400  
 Gln Gly Met Arg Pro Pro Met Pro Pro His Gly Gln Tyr Gly Gly His  
 405 410 415  
 His Gln Gly Met Pro Gly Tyr Leu Pro Gly Ala Met Pro Pro Tyr Gly  
 420 425 430

Gln Gly Pro Pro Met Val Pro Pro Tyr Gln Gly Gly Pro Pro Arg Pro  
 435 440 445

Pro Met Gly Met Arg Pro Pro Val Met Ser Gln Gly Gly Arg Tyr  
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<210> 37

<211> 1250

<212> DNA

<213> Homo sapiens

<400> 37

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tggaataata actggatttt cagaatattg ttgttttctg tagtgttcaa ggtattgttt 180
ctaaacataa acataactcta aacatgcttt attcacttgt taaagtcata cttttaaag 240
taatacctta ctaaagatgg tgattacttt tccgagggtca gaaaaggaaa gctaagcggt 300
ttcattatca aatacacaag cttattaaat gaatgactgt taactacttt attttcattt 360
gcacattaat tttggaattg tttctgtttt gctgctgacg gaaatactat tttggctctg 420
tgtatatttg tattttgatt tttctgggtt gtttaccctt atttgctttt agctccgcct 480
tatgttttaa tatattctaa cttatgtaaa gagcataatc ttagagcaaa aatacttgag 540
gttttatgtc agatctaata ttaagtgttt gttgtttttt aaaagggtgt ttctcagatg 600
gctgcagtgt ttttgctatt tctgcataaa taccctacct ggactcccca gttttcacca 660
gaaactgtta tttttttttg ttgttggtcc cactgagact gatggtgatg gggaaattaa 720
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<210> 38

<211> 90

<212> PRT

<213> Homo sapiens

<400> 38

```

Met Phe Lys Tyr Ile Leu Thr Tyr Val Lys Ser Ile Ile Leu Glu Gln
  1             5             10             15

Lys Tyr Leu Arg Phe Tyr Val Arg Ser Asn Leu Lys Cys Leu Leu Phe
      20             25             30

Phe Lys Arg Cys Phe Leu Arg Trp Leu Gln Cys Phe Cys Tyr Phe Cys
      35             40             45

Ile Asn Thr Leu Pro Gly Leu Pro Ser Phe His Gln Lys Leu Leu Phe
      50             55             60

Phe Phe Val Val Val Pro Thr Glu Thr Asp Gly Asp Gly Glu Ile Lys
      65             70             75             80

Asn Asn Thr Leu Ala His Ser His Lys Thr
      85             90

```

<210> 39  
 <211> 793  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
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 ccgcttcttc accatccctcg ggctgttctg cgcgggccag ggcgtcttct gggcttccat 180  
 ggctgtggca gccgtgtccc ggcccccggt tccggtgcag cctctggatg cggagggtccc 240  
 aaatcgtggc cccttcgacc tgcgtccgc gctctggcgc tacggtctgg ccgtcggctg 300  
 cggcgccatc ggagccctcg tactcgggtg tggctctctc ttctctctcc ggtctgtgcg 360  
 ctcagtgggt cttcgagctg gagggcagca ggtgacctc accactcatg ccccttttg 420  
 cttgggggccc catttcacag ttcctttgaa gcaggtatct tgcattggccc accggggtga 480  
 agtccctgcc atgctacctc tgaaagtcaa aggcgcagc ttctatttcc tcttgacaa 540  
 aactggacac ttccctaaca caaaactctt tgacaatact gtgggtgcct accggagctt 600  
 gtgaagaaat gacctcaagt cactcacctc tccaagagga ggataaaaac tgaaccttgg 660  
 ggagccagggt gtgttggttc acgctgttg taatcccagc actttgggag ggtgaggcag 720  
 gagcactgct cgagcccagg ctgggcaaca tagcgagacc ttgtctctat ttacaaaaaa 780  
 aaaaaaaaaaaa aaa 793

<210> 40  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
 Met Ala Val Ala Ala Val Ser Arg Pro Pro Val Pro Val Gln Pro Leu  
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 Asp Ala Glu Val Pro Asn Arg Gly Pro Phe Asp Leu Arg Ser Ala Leu  
 20 25 30  
 Trp Arg Tyr Gly Leu Ala Val Gly Cys Gly Ala Ile Gly Ala Leu Val  
 35 40 45  
 Leu Gly Ala Gly Leu Leu Phe Ser Leu Arg Ser Val Arg Ser Val Val  
 50 55 60  
 Leu Arg Ala Gly Gly Gln Gln Val Thr Leu Thr Thr His Ala Pro Phe  
 65 70 75 80  
 Gly Leu Gly Ala His Phe Thr Val Pro Leu Lys Gln Val Ser Cys Met  
 85 90 95  
 Ala His Arg Gly Glu Val Pro Ala Met Leu Pro Leu Lys Val Lys Gly  
 100 105 110  
 Arg Arg Phe Tyr Phe Leu Leu Asp Lys Thr Gly His Phe Pro Asn Thr  
 115 120 125  
 Lys Leu Phe Asp Asn Thr Val Gly Ala Tyr Arg Ser Leu  
 130 135 140

<210> 41  
 <211> 1970  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 41

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 taggagaatg actccgattc gtgacctca gcgccgtgc atgtcgatat atttattgag 120  
 tgtctactgt gtgccaggca ctatatctat gtgcatagaa aaaccctgga aggccgtaca 180  
 acaatatata tagagtgtac gtctctgtctt gctgagctaa cagcaagtgtt atttctgac 240  
 gtgaaagttag aagaagtctc acaaacagcc atttggaaaa aaagaagtgt gatgagtata 300  
 ttccaggtag aacctcctta ggcatgtctg tttttaacct aagcaacgcc attatgggca 360  
 gtgggatttt gggactcggc tttgccctgg caaacactgg aatcctactt tttctggtac 420  
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 aagaaacagg ctgcatgggt tatgaaaagc tgggggaaca agtctttggc accacagggg 540  
 agttcgtaat ctttgagacc acctctctac agaactctgg agcaatgctg agctacctct 600  
 tcatcgtaaa aatgaacta cctctgtcca taaagtgtct aatgggaaag gaagagacat 660  
 tttcagcctg gtacgtggat ggcgcgttc tgggtggtgat agttaccttt ggcataattc 720  
 tccctctgtg tctcttgaag aacttaggtt atcttggcta tactagtggg ttttcttga 780  
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 ttccagagct aaattcaaca ataagtgtta attcaacaaa tgctgacacg tgtacggcaa 900  
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&lt;210&gt; 42

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

Met Ser Val Phe Asn Leu Ser Asn Ala Ile Met Gly Ser Gly Ile Leu  
 1 5 10 15  
 Gly Leu Ala Phe Ala Leu Ala Asn Thr Gly Ile Leu Leu Phe Leu Val  
 20 25 30  
 Leu Leu Thr Ser Val Thr Leu Leu Ser Ile Tyr Ser Ile Asn Leu Leu  
 35 40 45  
 Leu Ile Cys Ser Lys Glu Thr Gly Cys Met Val Tyr Glu Lys Leu Gly  
 50 55 60  
 Glu Gln Val Phe Gly Thr Thr Gly Lys Phe Val Ile Phe Gly Ala Thr  
 65 70 75 80  
 Ser Leu Gln Asn Thr Gly Ala Met Leu Ser Tyr Leu Phe Ile Val Lys  
 85 90 95

Asn Glu Leu Pro Ser Ala Ile Lys Phe Leu Met Gly Lys Glu Glu Thr  
 100 105 110  
 Phe Ser Ala Trp Tyr Val Asp Gly Arg Val Leu Val Val Ile Val Thr  
 115 120 125  
 Phe Gly Ile Ile Leu Pro Leu Cys Leu Leu Lys Asn Leu Gly Tyr Leu  
 130 135 140  
 Gly Tyr Thr Ser Gly Phe Ser Leu Ser Cys Met Val Phe Phe Leu Ile  
 145 150 155 160  
 Val Val Ile Tyr Lys Lys Phe Gln Ile Pro Cys Ile Val Pro Glu Leu  
 165 170 175  
 Asn Ser Thr Ile Ser Ala Asn Ser Thr Asn Ala Asp Thr Cys Thr Pro  
 180 185 190  
 Lys Tyr Val Thr Phe Asn Ser Lys Thr Val Tyr Ala Leu Pro Thr Ile  
 195 200 205  
 Ala Phe Ala Phe Val Cys His Pro Ser Val Leu Pro Ile Tyr Ser Glu  
 210 215 220  
 Leu Lys Asp Arg Ser Gln Lys Lys Met Gln Met Val Ser Asn Ile Ser  
 225 230 235 240  
 Phe Phe Ala Met Phe Val Met Tyr Phe Leu Thr Ala Ile Phe Gly Tyr  
 245 250 255  
 Leu Thr Phe Tyr Asp Asn Val Gln Ser Asp Leu Leu His Lys Tyr Gln  
 260 265 270  
 Ser Lys Asp Asp Ile Leu Ile Leu Thr Val Arg Leu Ala Val Ile Val  
 275 280 285  
 Ala Val Ile Leu Thr Val Pro Val Leu Phe Phe Thr Val Arg Ser Ser  
 290 295 300  
 Leu Phe Glu Leu Ala Lys Lys Thr Lys Phe Asn Leu Cys Arg His Thr  
 305 310 315 320  
 Val Val Thr Cys Ile Leu Leu Val Val Ile Asn Leu Leu Val Ile Phe  
 325 330 335  
 Ile Pro Ser Met Lys Asp Ile Phe Gly Val Val Gly Val Thr Ser Ala  
 340 345 350  
 Asn Met Leu Ile Phe Ile Leu Pro Ser Ser Leu Tyr Leu Lys Ile Thr  
 355 360 365  
 Asp Gln Asp Gly Asp Lys Gly Thr Gln Arg Ile Trp Ala Ala Leu Phe  
 370 375 380  
 Leu Gly Leu Gly Val Leu Ser Pro Cys Gln His Ser Leu Val Ile Tyr  
 385 390 395 400  
 Asp Trp Ala Cys Ser Ser Ser Asp Glu Gly His  
 405 410

<210> 43  
 <211> 812  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
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 agggccaacc accgcaagga gctgaaggcg gcgggagccc gagtcgccgc cggcgtcggg 180  
 gccgtcaaag aagatggcca gggagacagc agcgtgggca gagtggtagg agctggccat 240  
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 ctactgtgg ttggtggg cggtgacaga gtgtgcagca cgaccagagt ggcttttctg 360  
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<210> 44  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Met Pro Gly Cys Trp Val Leu Glu Leu Val Asp His Trp Leu Ala Ser  
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 Leu Trp Leu Val Val Ala Val Thr Glu Cys Ala Ala Arg Pro Glu Trp  
 20 25 30  
 Leu Phe Trp Leu Cys Arg Pro Ala Ala Pro Cys Gln Glu Glu Glu  
 35 40 45  
 Thr Pro Arg Ala Cys Asp Thr Met Ala Arg Leu Ala Ala Gly Ser Thr  
 50 55 60  
 His Val Thr Asp Glu Glu Thr Lys Glu His Ser Tyr Leu Leu Thr Arg  
 65 70 75 80  
 Thr Arg Phe Glu Ala Glu Leu Arg Pro Val Glu Gln Lys Leu Ser Ala  
 85 90 95  
 Leu Gln Ser Pro Leu Ala Gln Arg Pro Phe Phe Glu Val Pro Ser Pro  
 100 105 110  
 Leu Gly Ala Val Asp Leu Tyr Glu Tyr Ala Cys Gly Asp Glu Asp Leu  
 115 120 125  
 Glu Pro Leu  
 130

<210> 45  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (360)

&lt;400&gt; 45

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ggatgctgag gccgcggaaa gtcagcctcc tcacccccca ggtacgaggc caggaagggg 240
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ggtgtaaaac tggtaaaaaa aaaaaaaaaa aaa 1533

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&lt;210&gt; 46

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (91)

&lt;400&gt; 46

```

Met Ser Val Val Phe Trp Leu Ser Gly Arg Pro Ser Lys Ser Gly Phe
  1             5             10             15

Phe Gly Pro Pro Arg Gln Glu Met Gly Ser Leu His Gly Arg Gln Asp
          20             25             30

Ala Glu Ala Ala Glu Ser Gln Pro Pro His Pro Pro Gly Thr Arg Pro
          35             40             45

Gly Arg Gly Arg Pro His Gln Cys Trp Val Pro Ala Pro Ala Ala Arg
          50             55             60

Leu Leu Gly Pro Ala Trp Leu Ala Ala Arg Ala Val Cys Leu Gln Lys
          65             70             75             80

Arg Gln Gly Pro Pro Cys Gln Ala Ser Ser Xaa Leu Pro Val Gly Ser
          85             90             95

```

Ala Cys Val Ser Ser Cys Arg Ile Ser Lys Leu Leu Lys Val His Leu  
 100 105 110

Leu Arg Gln Arg Gly Gln Val Gly Arg His Leu Cys Pro Leu Val Gln  
 115 120 125

Glu Gln Arg Gln Ala Ala Pro His Ser His Val Glu Ser Ser Gln Gly  
 130 135 140

Lys Gly Gly Cys Gly Gly Asp Arg Gly Arg Arg Pro Arg Ala Gly Thr  
 145 150 155 160

Ser Cys Ser His Gly Gly Arg Ser Trp Ser Leu Ser Ala Val Gly Ser  
 165 170 175

His Cys Leu Pro Ala Leu Pro Leu Ser Pro Ala Ala Pro Ala Pro Pro  
 180 185 190

Arg Arg Leu Ser Leu Ser Glu Lys Arg Arg Pro Ala Leu Gln Ser Gly  
 195 200 205

Ala Pro Ser Lys Ser Ala Glu Ala Gly Val Pro Thr Ser Thr Leu Glu  
 210 215 220

Val Ser Arg Arg Val Met Trp Gly Ala  
 225 230

&lt;210&gt; 47

&lt;211&gt; 3023

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

tcacattgcc aaaagacggc aatatgggtgg aaaataacat atagacaaac gcacaccggc 60  
 cttattccaa gcggcttcgg ccagtaacgt tagaattgcc gagaagtcac gataatttcg 120  
 tttgttcttc cagatttagg catatactta tttaatcaat aatgtgttaa cagctgacac 180  
 ctgtgggtgc tgtgacaggc actatttgaa gtgctttatc atggattaac tcttaatcct 240  
 cagctaccgt ataaagtagg acataacccc atttcacatg cactacactg agacttgcc 300  
 cctctccccc cacttggaag atgttctttt ttcataacta tatactatc cattgcatga 360  
 atattctgta atttatttaa tccccatagg attgataatt aggttcatta tagatagaag 420  
 tgtaattaac attcctgtac atgtattttg ctacttgtgt ggggtatttct gtaggatgaa 480  
 taactagaaa tttattggat cagggttcac atttgcagtt ttgaaaacta ctacacaaaa 540  
 gatttcacca atttacaact ccatcattag taagaatgcc tgtttgccta tagtctgcca 600  
 accctgaatc cttaaaaatt tttgccaatc tggtaggcaa aatttcttct ttttctttga 660  
 atattaatga ggaggaacat cttttcatgt ttcttgccca ttgcatctc ctattatgaa 720  
 ttgcttttgc ccattttcct ttttttaatt atgaaagtct aatgactacc ttctcattgt 780  
 ataaaaaaca cagttctttg aatagagaga cccttttctc caatgctacc aatcacattc 840  
 cacttaccac agtttaacat acatcctcta gtcaccttc cgtacgaata tacatacaca 900  
 taaaaacact ttttacataa ataggatctc atattctgta gctttttaaa attttggtct 960  
 caaaaaaaga taacaggtct ttaaatttct ttaatgggtg actatgatta aatactatga 1020  
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 aggtggattt ttggatcaaa gggtttgttc tctgtccacc ttcagctctc ccaaaggcct 1200  
 tcataactgt attttacca agtgatgga gaatgttcat tccccatat aaccatacct 1260  
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 gattataaaa aaaaatgggt agattggggt tattttcatg tttattggcc atttatagtt 1380  
 tactgtggat tgtttgtatc ccttacctgc ttctattgg gttatgtgtg gatataattg 1440  
 ttttatttgt tcagcatctc cttcccatc ttctggtaac acaaccttta tttatttgg 1500

```

gggaacctat tccctgtggc ttaggtgagc atgtgaccag gcctggcctc ctgagtccca 1560
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gtattttctt attgatttgt agaaaacctt gtaattttaa attctagact ttatgcccta 1980
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acgcctgttc tcaactgcatg tcttctgtgt tgtactgaag ctctagctg gtgcagtga 2160
gcaagacaaa gaaaggaaat ataggtgcac tgggaaggaa gaagaaacac tgcctttatt 2220
ctttagggtga catgattgtg tgcttttaaa ataataaagg aatcaacaga aaagttgctt 2280
aacctaataa atgagtttat caaagtcaca agatacaagg tcagtataca aaaatcagtt 2340
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accttgatgg atggaagcct taaggtaaag atgctcattc tccccacac gacctgtaca 2520
ttccccacag gcctaataca aacccccaca ggcttctgtg tagaaattga catgctgac 2580
ctgaaattta tatgaaatg caaagagtct ggaataacca aaataatttt gtaaaagaac 2640
aaagaagact tctactacct ggttataaga cttctctgaa gcacagaagt caaggcagt 2700
tggtggtggc ataagtaatg taaatcatcc aggtgtggtg gctcaggcca gtcattccagc 2760
actttgggag gctgaggcag gagaatcgct agagcccagg agttggaaac cagcctgggc 2820
agcatagcaa gactcatctc tacaaaaaat acgaaacaat tagctgggtg tctgtagcac 2880
atgcctgtag tcccagctgc gcgggaggct gagctgggaa gatcacttta gcctgggaa 2940
tcagggggagc tgtgatcaca ccactgcact ccagcctggg caacagagca agaccccatc 3000
tcaaaaacaa aaaaaaaaaa aaa 3023

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&lt;210&gt; 48

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

```

Met Lys Met Pro Leu Phe Ile Pro Leu Ile Phe Phe Pro Leu Ala Ile
  1             5             10            15

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Thr Leu Pro Lys Leu Thr Ser Tyr Ser Asp Val Phe Val His Val Cys
          20             25            30

```

```

Glu Tyr Phe Phe Ser Leu Glu Ser Ser Lys Val Asp Phe Trp Ile Lys
    35             40            45

```

```

Gly Phe Val Leu Cys Pro Pro Ser Val Phe Pro Lys Ala Phe Ile Thr
    50             55            60

```

```

Val Phe Ser Pro Ser Val Trp Arg Met Phe Ile Ser Pro Tyr Asn His
    65             70            75            80

```

Thr Tyr Thr

&lt;210&gt; 49

&lt;211&gt; 1049

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

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gtaactatct ccatgtttgt ccttttctac ctggtttttt caccactccc aacataacc 60
tcccaatctt ttttgtagt ccggccgtca atttgtagt taccaatttc tgtaaattct 120

```

```

ctcaattcat tgaagatcgt aggggttaaac ttttttgtgt gtgattttaa cttacaaaca 180
agtgaagaag ctatcggtta tttcagacga ggctgtagtt taaataccaa aagagggaaa 240
ataaaaaaga acctttgtaa aatataatctg aacctaatgg tttgtacact ggagaatcgt 300
tctagatagt taccaattaa atataactcc gccagtgtaa ggggtgtgagg tgcagttgtc 360
caggagacga ttttgtatag tatttttctt gtacattact tccagtaa atttgaaaat 420
atattgaagt aaacttgatt tttttttgt cacaagaaaa tattaagagt tattgttgca 480
gttctgatga gctgcagggt ttttgaactc acttctggag gtgcagagcc acaaacgcac 540
tttcggggcc tagttttgct cgaatatgaa tttagatagg tatcaagctg taactaagac 600
aatatttgat aaatgttggg tgacatttaa tttaatggag catgtactta tttgcatttg 660
ctggcagttc aggcatagtt aaagtggag ttctccgata tttcataata agtgggtctg 720
ccaaaaccca tgtattaaat aaattgtcca agtgaaactc gactaacttt ggcctttgtg 780
tatttcttga aggtaatatt gttaactgtt aataaatact tctgacacta catttaaatg 840
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tgaaatgaa aagcctttct ctggagcatt ttagatttgc attttaaatg catgaaatgt 960
aattgattta tttgtaaaat tttaatggg gtaataaac tcagaaaaaa aaaaaaaaaa 1020
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1049

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&lt;210&gt; 50

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

```

Met Phe Val Leu Phe Tyr Leu Val Phe Ser Pro Leu Pro Asn Ile Thr
  1             5             10             15

Ser Gln Ser Phe Leu Leu Val Arg Pro Ser Ile Cys Ile Val Pro Ile
      20             25             30

Ser Val Asn Ser Leu Asn Ser Leu Lys Ile Val Gly Leu Asn Phe Phe
      35             40             45

Val Cys Asp Leu Asn Leu Gln Thr Ser Glu Glu Ala Ile Val Tyr Phe
      50             55             60

Arg Arg Gly Cys Ser Leu Asn Thr Lys Arg Gly Lys Ile Lys Lys Asn
      65             70             75             80

Leu Cys Lys Ile Tyr Leu Asn Leu Met Val Cys Thr Leu Glu Asn Arg
      85             90             95

Ser Arg

```

&lt;210&gt; 51

&lt;211&gt; 1707

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 51

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cacacagctc ccggatgaag ataacagttg gtagaccaa aggtgacctc gcttagtata 60
ttgaaaacac acaccacaca tcacacacag aactgaatca taccacgtgc tgcctatggg 120
acttcagtta ctgtttcctg agttactgtt tatccgctgg caatggtgtg atttgtctgg 180
atcagatccg tgctattccc caaccacct ccagataatg tgagaaaata gccatgtcag 240
tatgtaggaa ctctgatggt gctcagattt gtgtgttcaa tcaatgggct taaatcagca 300
aaatattatg cctaaagtaa atctgttctt aacaagggct ctaccactgc attttcacat 360
gtaccttcag ggggttatct tttttttttt cccctcctat tttaatcagc aaaatccata 420
ccaaaacaac gacaacaacg ccctcttaag ggaccacct ttggtcaatc ataacatgct 480
gtttaagca gctgtttaca ggatgtgtag tggatgccc ttgtcatata ctcttagcat 540

```

```

atcttttttt cctttggcct tgcattgctt tcttcaggta ctgtctcggt atcattctgc 600
taatcattgt tacagaatgg tgacttcatt tgtgctaaca gtacaacagc agatttgggt 660
caggcttaat ctagtgtaa cttttttttt tgggtgcttt ttggattgat gactgtctca 720
ctttgactat acccatgttt tgcattgcaat gactcatgca tggttttctt aactagctaa 780
tattaacaat ttattccata taaaaatgga attttgcaac atcctttaat aaggtgaggg 840
aagcatgaac ctcagacttc tggcactatt acatagtaag cacatgaagt agtttgataa 900
taaatagcag ttctagtact tcacatttca cccgtgtgtg caatgccttt ttctgggggg 960
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agaaaagtga aattgaaaat accaaaagat gtatcatttt tatttgaatc catcatgcag 1140
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tatgtgcact gtgtatctta tatgaatgtt ttattttata taccacatgc aaaaatgtcc 1260
atatgcaacta tttaaagtgt ttaaataata tattccttct ttataatgct aaatctatat 1320
gagtaccata tttttataag tcagtgtgtc gactggtttc attttagaat taacagctgc 1380
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cagcacttat gctctgtgac agtattgtgt gtcattgttg agcagtatgt ggtagaatta 1500
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tatatagata tatatgtcca ccagtataat ggcattgctg tgtctggcac ttcattgtac 1620
ggacttttat aataaaaagaa cttgaaagtt tttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1707

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&lt;210&gt; 52

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

```

Met Gly Leu Asn Gln Gln Asn Ile Met Pro Lys Val Asn Leu Phe Leu
  1             5             10             15

Thr Arg Ala Leu Pro Leu His Phe His Met Tyr Leu Gln Gly Val Ile
      20             25             30

Phe Phe Phe Phe Pro Ser Tyr Phe Asn Gln Gln Asn Pro Tyr Gln Asn
  35             40             45

Asn Asp Asn Asn Ala Leu Leu Arg Asp His Pro Leu Val Asn His Asn
  50             55             60

Met Leu Phe Lys Ala Ala Val Tyr Arg Met Cys Ser Gly Met Pro Leu
  65             70             75             80

Ser Tyr Thr Leu Ser Ile Ser Phe Phe Pro Leu Ala Leu His Gly Phe
      85             90             95

Leu Gln Val Leu Ser Arg Tyr His Ser Ala Asn His Cys Tyr Arg Met
  100            105            110

Val Thr Ser Phe Val Leu Thr Val Gln Gln Gln Ile Trp Val Arg Leu
  115            120            125

Asn Leu Val Leu Thr Phe Phe Ser Gly Ala Phe Leu Asp
  130            135            140

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&lt;210&gt; 53

&lt;211&gt; 1922

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 53

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aaagcaccag gaactggttg accacctttc ccagcatgtc tcttaggggc ctgacctcag 60
gatttcagac tggattcact gtgacagaac taagggaata aatacatttt atgtccacgt 120
tcccactctg gtgtaccatc tgtccacaga ggggagagaa caagcaagag gttgggggtg 180
gccatccagt gtcccctgga gcagaccttg gcctctggtc ttcagtcccc ggctcctctg 240
tctgtgtgtc ggccctggtg ggaagccctg acttgtaact ctcaaagcct aacttcaggg 300
gttgccctgc cagtgccttc tccgggagct ttgggtccct gggtataagc tttcagttct 360
cagtgtctgc tgtcaccagt aaccaagtgc tgaaaatgat ctgtaccact ttgtgacaa 420
gggcggtctg gccagggtgc ccccgcccag ctctctctac tctccctgtg gcctggggct 480
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atgatttaag caaacttaaa actcaatgct ttattgatag tttaaataat taacattacg 600
taaagaaaaa tctaaatgta aacagttttt gcaaacgagt atccattaa ggaacttcaa 660
gtacctaacc cctattaaac aatttatgta aaccactctt ccttaaagaa aatcgaatgc 720
ccagctcctt cccaatcttc caagctctga agtagggaag aggtgcagct aggagcagat 780
ggggcagtggt gtgtgttgga ggtggaggag tgggggaaat caaatcagct cacctgtgtg 840
gttatttate agtgaacttt aataaactgg tactgggaaa gaaaaggagg ctagtgtattg 900
acagcatccc gggctgctga gaggaccagc atgatgagct gtcttggagt tggcaattag 960
gagctcgtga gcgacctttg ccagaacagt tccatgggac gacctggctg gaggcctaatt 1020
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ctgaacatat gcacaggac gcataatggg gctttgttcg ggcctgggca gacatggagg 1140
gcaatgcctg agctctcttc cagtttatct ccacgtcctc caagctcaaa tctggcagcc 1200
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tgaacccaag aggcggaggt tgcagtgagc aggtatcacg ccaatgcacc ccagcctggg 1860
caacaaagcg agaattctgtc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aa
1922

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&lt;210&gt; 54

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

```

Met Gly Leu Cys Ser Gly Leu Gly Arg His Gly Gly Gln Cys Leu Ser
  1              5              10             15

Ser Leu Pro Val Tyr Leu His Val Leu Gln Ala Gln Ile Trp Gln Pro
      20              25              30

Trp Ser Gly Leu Lys Leu Lys Leu His Arg Ala Val Asp Leu Met Leu
      35              40              45

Gln Arg Cys Val Asp Ile Gln Pro Leu Ser Leu Ala Pro Lys Cys Pro
      50              55              60

Trp Glu Leu Leu Ser Phe His Gly Asp Asp Pro Arg Pro Trp Val Ser
      65              70              75             80

Pro Ala Ser Ser His Ser Val Lys Thr Thr Gln Leu Leu Leu Leu Glu
      85              90              95

Ile Ile Leu Glu Phe Leu Gly Gln Pro Leu Phe Lys Ala Leu Cys Val

```

100

105

110

Pro Asp

&lt;210&gt; 55

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

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tttttccaca ctcagctttc ccctagcatg gacaagattt tcagccattt ttgccacata 60
tacattttta agggaaaaag atttttctct gtaagaaagt tctggttatg ctgtttttaa 120
ggtgacttgt caggagttga gacttccctg ccggattcta ttttgaaagt aaatggctt 180
ccctccttgt tccgattctg cggtcccatc gtcagacaac tttggagtat tagaaaccac 240
tgtatatatg tggaaagcca ggtcagccag actgttagat tgggtgtgcac tcacctgaga 300
gatctggcag gttggatata tttatgtgta tttctccaca gtgcttgctt tgccctgttg 360
gtaaggattt taaataacca tgctcaaaag agctgttcta atctgcgttt tgcattgtaa 420
gtgttaatat caaacattct taacgtgctc gaggaattgc ttttaacatt ctactttgcc 480
agtttcttca ttagattaat tgacatgtat tatttaaagt accagtgatg ctttgtgcaa 540
ttatgaatgt tgaagattaa agtacatagt tactaaaaaa aaaaaaaaaa 589

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&lt;210&gt; 56

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

```

Met Asp Lys Ile Phe Ser His Phe Cys His Ile Tyr Ile Phe Lys Glu
  1             5             10             15

Lys Arg Phe Phe Ser Val Arg Lys Phe Trp Leu Cys Cys Phe Lys Gly
          20             25             30

Asp Leu Ser Gly Val Glu Thr Ser Leu Pro Asp Ser Ile Leu Lys Val
          35             40             45

Asn Gly Leu Pro Ser Leu Phe Arg Phe Cys Val Pro Ile Val Arg Gln
          50             55             60

Leu Trp Ser Ile Arg Asn His Cys Ile Tyr Val Glu Ser Gln Val Ser
          65             70             75             80

Gln Thr Val Arg Leu Val Cys Thr His Leu Arg Asp Leu Ala Gly Trp
          85             90             95

Ile Tyr Leu Cys Val Phe Leu His Ser Ala Cys Phe Ala Leu Leu Val
          100            105            110

Arg Ile Leu Asn Asn His Ala Gln Lys Ser Cys Ser Asn Leu Arg Phe
          115            120            125

Ala Cys
          130

```

&lt;210&gt; 57

&lt;211&gt; 1363

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

```

gtagtggact tgatcttctt taacacagaa gtgtcactgt cacaagcctt ggaggatgtt 60
agcaggggag gttctctctt tgctattgtc atcaccagc aacaccagat tcaccgctcc 120
tgcacagtca acatcatgtt tggaaacccc caagagcatc gcaacatgcc ccaagcagat 180
gccatggtgc tggtagccag aaattatgag cgttacaaga atgagtgccg ggagaaggaa 240
cgtgaggaga ttgccagaca ggcagccaag atggccgatg aagccatcct gcaggaaaga 300
gagagaggag gccctgagga gggagtgcgt gggggccacc ctccagccat ccagagcctc 360
atcaacctgc tggcagacaa caggtacctc actgctgaag agactgacaa gatcatcaac 420
tacctgcgag agggaggag cggctgatga ggagcagcac cgactctctg cctggggagc 480
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tagccagacc acagcacaga tggggcagcc acaggccccc atgggatctt accagaggca 1080
ttactgagag ctaaattctt caactctccc cagtccctc atccccctgc ctctctccc 1140
ttacttggtc taaatagagc tgtttgagg atgttctctg cgctcccagg ccggcatcga 1200
gtgtcatcaa tttctaccac ctgtctctc tttgccccaa ggctgtgttg cttattcctt 1260
acaagttta tactgcattt ggggtgtat cttttttgt tttttgttt gtagaaaata 1320
aaaatctccg ggggcaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1363

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&lt;210&gt; 58

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

```

Met Leu Ala Gly Glu Val Leu Leu Leu Leu Ser Ser Pro Ser Asn
 1              5              10              15

Thr Arg Phe Thr Ala Pro Ala Gln Ser Thr Ser Cys Leu Glu Pro Arg
 20              25              30

Lys Ser Ile Ala Thr Cys Pro Lys Gln Met Pro Trp Cys Trp Trp Pro
 35              40              45

Glu Ile Met Ser Val Thr Arg Met Ser Ala Gly Arg Arg Asn Val Arg
 50              55              60

Arg Leu Pro Asp Arg Gln Pro Arg Trp Pro Met Lys Pro Ser Cys Arg
 65              70              75              80

Lys Glu Arg Glu Glu Ala Leu Arg Arg Glu Cys Val Gly Ala Thr Leu
 85              90              95

Gln Pro Ser Arg Ala Ser Ser Thr Cys Trp Gln Thr Thr Gly Thr Ser
100              105              110

Leu Leu Lys Arg Leu Thr Arg Ser Ser Thr Thr Cys Glu Arg Glu Gly
115              120              125

Ala Ala Asp Glu Glu Gln His Arg Leu Ser Ala Trp Gly Ala Thr Trp
130              135              140

```

Gln Gly Arg Gly Pro Ile Ser Arg Gln Pro Leu Gly Ala Thr Ser Gly  
 145 150 155 160  
 Ala Ser Leu Lys Thr Gln Pro Ser Ser Gln Pro Leu Gln Ser Gly Gln  
 165 170 175  
 Val Leu Pro Ser Ala Thr Pro Thr Pro Ser Ala Pro Pro Thr Ser Gln  
 180 185 190  
 Gln Glu Leu Gln Ala Lys Ile Leu Ser Leu Phe Asn Ser Gly Thr Val  
 195 200 205  
 Thr Ala Asn Ser Ser Ser Ala Ser Pro Ser Val Ala Ala Gly Asn Thr  
 210 215 220  
 Pro Asn Gln Asn Phe Ser Thr Ala Ala Asn Ser Gln Pro Gln Gln Arg  
 225 230 235 240  
 Ser Gln Ala Ser Gly Asn Gln Pro Pro Ser Ile Leu Gly Gln Gly Gly  
 245 250 255  
 Ser Ala Gln Asn Met Gly Pro Arg Pro Gly Ala Pro Ser Gln Gly Leu  
 260 265 270  
 Phe Gly Gln Pro Ser Ser Arg Leu Ala Pro Ala Ser Asn Met Thr Ser  
 275 280 285  
 Gln Arg Pro Val Ser Ser Thr Gly Ile Asn Phe Asp Asn Pro Ser Val  
 290 295 300  
 Gln Lys Ala Leu Asp Thr Leu Ile Gln Ser Gly Pro Ala Leu Ser His  
 305 310 315 320  
 Leu Val Ser Gln Thr Thr Ala Gln Met Gly Gln Pro Gln Ala Pro Met  
 325 330 335  
 Gly Ser Tyr Gln Arg His Tyr  
 340

&lt;210&gt; 59

&lt;211&gt; 1613

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

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 aatagtttca tcttttggt catcgaaaaa gtcagctctg attcatccat atccaataaa 360  
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 acatggcaag accccatctc cgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1613

&lt;210&gt; 60

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

Met Asp Arg Val Phe Arg Ala Thr Cys Leu Leu Phe Leu Lys Phe Pro  
 1 5 10 15  
 Gly Gly Ala Ser Ser Gly Pro His Ile Ser Ser Val Pro Ser Gln Arg  
 20 25 30  
 Asn Thr Ser Asp Pro Ser Ser Leu Pro Trp His Ile Thr Pro Trp Ser  
 35 40 45  
 Leu Asp Ala Ser Ser Phe Trp Ser Ser Glu Ser Phe Leu Ser Ser Ser  
 50 55 60  
 Val Thr Gly Val Gly Gly Leu Ser Thr Leu Pro Ser Arg Met Cys Leu  
 65 70 75 80  
 Phe Gln Ser Ile Gly Thr Thr Pro Cys Ser Pro Val Thr His Val Pro  
 85 90 95

&lt;210&gt; 61

&lt;211&gt; 1700

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 61

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 ctggaggccg agctggggcc ctcacctcgc gctcccagc tgtagagtt caccgaccat 120  
 ggaggcagtg gcttcgtggg cggcctctgc cagggtggcg cggcctacca ggagctgttt 180  
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 cgctattttg cgtggtgga gcggcggtg gcgcaggagc aggggtggtg tgacaactca 300  
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 cagggtgtcc gtgaggccct catcgtgggc ttcgtccact ctatgttcca gacggctcag 720  
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&lt;210&gt; 62

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

Met Glu Ala Val Ala Ser Trp Ala Ala Ser Ala Arg Trp Arg Arg Pro  
 1 5 10 15

Thr Arg Ser Cys Leu Arg Pro Arg Ala Gln Gln Val Pro Arg Ser Trp  
 20 25 30

Arg Pro Ser Pro Gly Ser Trp Ala Ala Ala Ile Leu Arg Trp Trp Ser  
 35 40 45

Gly Gly Trp Arg Arg Ser Arg Val Val Val Thr Thr His Cys Trp Cys  
 50 55 60

Gly Arg Trp Thr Ala Ser Thr Gly Ala Cys Gly Leu Pro Gly Pro Cys  
 65 70 75 80

Trp Pro Leu Pro Gly Ser Gln Thr Leu Pro Arg Arg Ser Trp Asn Glu  
 85 90 95

Trp Pro Ala Ser Ala Trp Ala Thr Thr Cys Arg Val Ser Gly Arg Pro  
 100 105 110

Ser Trp Ala Ala  
 115

&lt;210&gt; 63

&lt;211&gt; 1616

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (869)

&lt;400&gt; 63

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 taccagaagt atcaactcag gaacaatttt ctactagctg agcctcagaa gcagcaactt 180  
 ttccaaagtg aagtgatgaa tggaggcgcc agccctctc ctcagggttaa gaaaggcaaa 240

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tcatagacgt cacattattt atttattttg aaaattcttc ttttagtcaa acttataagt 600
tttctgtggc tcaaaatatt ctcaaccagg gtttcttttag tggccatcag ctcccagggg 660
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&lt;210&gt; 64

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

```

Met Glu Lys Val Val Glu Gly Val Gly Pro Leu Phe Thr Tyr Met Leu
  1             5             10             15

Pro Ser Pro Pro Thr Asp Val Ile Ser Phe Ile Phe Val Thr Pro Val
      20             25             30

Asn Pro Arg Leu Gly Gly Phe Thr Pro Cys Ile Gly Thr Pro Leu Glu
      35             40             45

Ser Gly Leu Ala Cys Asp Phe Asn Gln Cys Lys Ala Glu Val Gly Ser
      50             55             60

Val Pro Val Leu Arg Leu Gln Arg Glu Arg Lys Val Gln Pro Ser Asn
      65             70             75             80

Ile Pro Ala Asp Ile Arg Pro Gln Leu Cys His Gln Leu His Ala His
      85             90             95

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Glu

&lt;210&gt; 65

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

```

gattgccgga agctgaaggg atgctttgaa cgtggggggg ctgcgtcaca gttggactcc 60
cacttgcaga ggacctgatt atgtccagt accacctgaa caacagcaca ctgaaggagg 120

```

```

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tctccacgcg gtccttcatc aaccgcccga accagagccg gaggcgggag gacggggtgc 300
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cgtgcacttc agctggagaa agaaaccaag aagggaa 937

```

&lt;210&gt; 66

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

```

Met Ser Ser Asp His Leu Asn Asn Ser Thr Leu Lys Glu Ala Gln Phe
 1             5             10             15

Lys Asp Leu Phe Leu Lys Lys Ala Glu Leu Glu Phe Ala Gln Ile Ile
 20             25             30

Ile Ile Val Val Val Val Thr Val Met Val Val Val Ile Val Cys Leu
 35             40             45

Leu Asn His Tyr Lys Val Ser Thr Arg Ser Phe Ile Asn Arg Pro Asn
 50             55             60

Gln Ser Arg Arg Arg Glu Asp Gly Leu Pro Gln Glu Gly Cys Leu Trp
 65             70             75             80

Pro Ser Asp Ser Ala Ala Pro Arg Trp Gly Ala Ser Glu Ile Met His
 85             90             95

Ala Pro Arg Ser Arg Asp Arg Phe Thr Ala Pro Ser Phe Ile Gln Arg
100             105             110

Asp Arg Phe Ser Arg Phe Gln Pro Thr Tyr Pro Tyr Val Gln His Glu
115             120             125

Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro
130             135             140

Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln
145             150             155             160

Met Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile
165             170             175

Phe Asp Ser Asp Leu Ile Asp Ile Ala Met Tyr Ser Gly Gly Pro Cys
180             185             190

Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Ser Thr Cys Ser Ser Asn
195             200             205

```



Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Met Gly His  
210 215 220

His Pro Gly Ala Ser Phe Leu His His Gln Arg Ser Asn Ala His Arg  
225 230 235 240

Gly Ser Arg Leu Gln Phe Gln Gln Asn Asn Ala Glu Ser Thr Ile Val  
245 250 255

Pro Ile Lys Gly Lys Asp Arg Lys Pro Gly Asn Leu Val  
260 265

<210> 67

<211> 1467

<212> DNA

<213> Homo sapiens

<400> 67

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gtaataatgg ttatgaaagc acttccaaca attctaaga tgataaaaca gtggatgatc 480
cactgttgca caaaattcta gcaacaatt ctaattcagc cacacttggt cttaataaca 540
gattgctctg tttttcataa ttattctaca tattaatata actgtgaagt cattacaaca 600
gctgtgtttt ttgggtcaca gatgttttat tttcaaagaa aacaaaattg tgtacgtttt 660
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1467

```

<210> 68

<211> 81

<212> PRT

<213> Homo sapiens

<400> 68

Met His Phe His Pro Leu Arg Leu Gln Val Lys Cys His His Thr Ala  
1 5 10 15

Ala His Pro Arg Glu Pro Gly Leu Pro Ala Ser Arg Ser Ser His Asp  
20 25 30

Val Gln Glu Lys Ala Leu Ser Lys Phe Asn Phe Pro Leu Phe Phe Phe  
35 40 45

Leu Glu Leu Phe Leu Ile Val Gln Arg Phe Pro Asp Asn Ser Phe Ser  
 50 55 60

Ile Ser Phe Ile Ala Ile Ser Ala Leu Ser Ser Ser Thr Glu Pro Gln  
 65 70 75 80

Leu

<210> 69

<211> 1235

<212> DNA

<213> Homo sapiens

<400> 69

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```

<210> 70

<211> 118

<212> PRT

<213> Homo sapiens

<400> 70

```

Met Ser Lys Pro Leu Ser Tyr Met Thr Trp Leu Phe Leu Leu Pro Ser
  1 5 10 15
Pro Leu Val Phe Val Ser Leu Phe Ser Pro Leu Ala Leu Leu Ala Leu
  20 25 30
Leu Trp Leu Cys Glu Gly Val Val Phe Ser Leu Gly Pro Cys Arg Cys
  35 40 45
Val Cys Gly Ser Arg Pro His Arg Pro Gln Arg Ala Gly Gln Arg Pro
  50 55 60
Glu Arg Pro Ser Glu Ala Arg Arg Arg Glu Pro Ser Gly Asp Glu Gln
  65 70 75 80
Glu Ala Ala Glu His Ala Gly Gly Ala Ala His Gln Glu Tyr Ala Leu

```

85

90

95

Ala Gln Gly Tyr Gly Ser Ser Val Pro Gly Asn Cys Ala Ala Gln Gln  
 100 105 110

Gly Val Arg Gly Ala Ser  
 115

&lt;210&gt; 71

&lt;211&gt; 835

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

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&lt;210&gt; 72

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr  
 1 5 10 15  
 Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro  
 20 25 30  
 Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile  
 35 40 45  
 Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly  
 50 55 60  
 Phe Asp Pro Arg His Gly Ser His Asn Ile Lys Lys Lys Ala Trp Tyr  
 65 70 75 80  
 Leu Ile Ala Met Leu Leu Lys Leu Ala Phe Cys Leu Ala Leu Cys Ala  
 85 90 95  
 Lys Leu Glu Gln Phe Thr Thr Met Asn Leu Ser Tyr Val Phe Ile Pro  
 100 105 110  
 Leu Trp Ala Leu Leu Ala Gly Ala  
 115 120

<210> 73  
 <211> 1287  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
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 gggaaacact taaggaataa atatggagct ggggtttaac actaaaacta gaaataaaca 1260  
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<210> 74  
 <211> 325  
 <212> PRT  
 <213> Homo sapiens

<400> 74  
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 Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys Ala  
 35 40 45  
 Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly Leu  
 50 55 60  
 Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu Val  
 65 70 75 80  
 Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu Leu  
 85 90 95  
 Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu Val  
 100 105 110  
 Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Glu  
 115 120 125

Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala Gly  
 130 135 140  
 Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp Lys  
 145 150 155 160  
 Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys Ala  
 165 170 175  
 Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala Ile  
 180 185 190  
 Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr Ala  
 195 200 205  
 Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala Glu  
 210 215 220  
 Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr Ile  
 225 230 235 240  
 His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg Tyr  
 245 250 255  
 Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu Val  
 260 265 270  
 Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val Ile  
 275 280 285  
 Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu Ala  
 290 295 300  
 Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu Arg  
 305 310 315 320  
 Lys Ser Lys Asn Ser  
 325

&lt;210&gt; 75

&lt;211&gt; 1396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 75

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aaaaaaaaaa aaaaaa 1396

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&lt;210&gt; 76

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

```

Met Ser Gln Ser Arg His Arg Ala Glu Ala Pro Pro Leu Glu Arg Glu
  1             5             10             15

```

```

Asp Ser Gly Thr Phe Ser Leu Gly Lys Met Ile Thr Ala Lys Pro Gly
      20             25             30

```

```

Lys Thr Pro Ile Gln Val Leu His Glu Tyr Gly Met Lys Thr Lys Asn
      35             40             45

```

```

Ile Pro Val Tyr Glu Cys Glu Arg Ser Asp Val Gln Ile His Val Pro
      50             55             60

```

```

Thr Phe Thr Phe Arg Val Thr Val Gly Asp Ile Thr Cys Thr Gly Glu
      65             70             75             80

```

```

Gly Thr Ser Lys Lys Leu Ala Lys His Arg Ala Ala Glu Ala Ala Ile
      85             90             95

```

```

Asn Ile Leu Lys Ala Asn Ala Ser Ile Cys Phe Ala Val Pro Asp Pro
      100            105            110

```

```

Leu Met Pro Asp Pro Ser Lys Gln Pro Lys Asn Gln Leu Asn Pro Ile
      115            120            125

```

```

Gly Ser Leu Gln Glu Leu Ala Ile His His Gly Trp Arg Leu Pro Glu
      130            135            140

```

```

Tyr Thr Leu Ser Gln Glu Gly Gly Pro Ala His Lys Arg Glu Tyr Thr
      145            150            155            160

```

```

Thr Ile Cys Arg Leu Glu Ser Phe Met Glu Thr Gly Lys Gly Ala Ser
      165            170            175

```

```

Lys Lys Gln Ala Lys Arg Asn Ala Ala Glu Lys Phe Leu Ala Lys Phe
      180            185            190

```

```

Ser Asn Ile Ser Pro Glu Asn His Ile Ser Leu Thr Asn Val Val Gly
      195            200            205

```

```

His Ser Leu Gly Cys Thr Trp His Ser Leu Arg Asn Ser Pro Gly Glu
      210            215            220

```

```

Lys Ile Asn Leu Leu Lys Arg Ser Leu Leu Ser Ile Pro Asn Thr Asp

```

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<210> 77
<211> 1238
<212> DNA
<213> Homo sapiens
```

```
<210> 78
<211> 385
<212> PRT
<213> Homo sapiens
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<400> 78

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Glu	Asp	Glu	Ile	Ile	Val	Pro	Lys	Lys	Lys	Leu	Val	Asp	Pro	Val	Ala
			20					25					30		
Gly	Ser	Gly	Gly	Pro	Gly	Ser	Arg	Phe	Lys	Gly	Lys	His	Ser	Leu	Asp
		35					40					45			

Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp  
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 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
 65 70 75 80  
 Ser Glu Gly Gly Val Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met  
 85 90 95  
 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp  
 100 105 110  
 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile  
 115 120 125  
 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu  
 130 135 140  
 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly  
 145 150 155 160  
 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg  
 165 170 175  
 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln  
 180 185 190  
 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln  
 195 200 205  
 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg  
 210 215 220  
 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His  
 225 230 235 240  
 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala  
 245 250 255  
 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu  
 260 265 270  
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu  
 275 280 285  
 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met  
 290 295 300  
 Gln Thr Gly Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg  
 305 310 315 320  
 Lys Leu Gly Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp  
 325 330 335  
 Val Asp Leu Tyr Thr Gly Ala Gly Trp Gly Pro Ser Leu Val Gly Pro  
 340 345 350  
 Ser Phe Leu Asp Phe Val Glu Glu Ala Pro Ser Val Ser Gly Ser Ala  
 355 360 365



Gly Asn Trp Arg Pro Phe Phe Ser Gln Phe Pro Phe Pro Asn Lys Ser  
 370 375 380

Leu  
 385

<210> 79  
 <211> 1558  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (1488..1489)

<400> 79  
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 gaagtgtgtg catcagctga cacttcaggt gcttgatttt gtgcaggatc cgtgctttgc 180  
 ccaaggagat ggtctcatta agctttatga aaactttatc agtgaatttg aacacagggt 240  
 gaaccctttg tccctcgtgg aaatcattct tcatgtagtt agacagatga ctgaccta 300  
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 gatcctgtgt aaaacagcaa ttggagctct aaaattaaac atcggggacc tacagggttac 420  
 aaaggaaaca attgaagatg ttgaagaaat gctcaacaac cttcctggtg tgacatcggt 480  
 tcacagtcgt ttctatgatc tctccagtaa atactatcaa acaatcggaa accacgcgtc 540  
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<210> 80  
 <211> 376  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
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 Leu Trp His Gln Leu Thr Leu Gln Val Leu Asp Phe Val Gln Asp Pro  
 35 40 45

Cys Phe Ala Gln Gly Asp Gly Leu Ile Lys Leu Tyr Glu Asn Phe Ile  
 50 55 60  
 Ser Glu Phe Glu His Arg Val Asn Pro Leu Ser Leu Val Glu Ile Ile  
 65 70 75 80  
 Leu His Val Val Arg Gln Met Thr Asp Pro Asn Val Ala Leu Thr Phe  
 85 90 95  
 Leu Glu Lys Thr Arg Glu Lys Val Lys Ser Ser Asp Glu Ala Val Ile  
 100 105 110  
 Leu Cys Lys Thr Ala Ile Gly Ala Leu Lys Leu Asn Ile Gly Asp Leu  
 115 120 125  
 Gln Val Thr Lys Glu Thr Ile Glu Asp Val Glu Glu Met Leu Asn Asn  
 130 135 140  
 Leu Pro Gly Val Thr Ser Val His Ser Arg Phe Tyr Asp Leu Ser Ser  
 145 150 155 160  
 Lys Tyr Tyr Gln Thr Ile Gly Asn His Ala Ser Tyr Tyr Lys Asp Ala  
 165 170 175  
 Leu Arg Phe Leu Gly Cys Val Asp Ile Lys Asp Leu Pro Val Ser Glu  
 180 185 190  
 Gln Gln Glu Arg Ala Phe Thr Leu Gly Leu Ala Gly Leu Leu Gly Glu  
 195 200 205  
 Gly Val Phe Asn Phe Gly Glu Leu Leu Met His Pro Val Leu Glu Ser  
 210 215 220  
 Leu Arg Asn Thr Asp Arg Gln Trp Leu Ile Asp Thr Leu Tyr Ala Phe  
 225 230 235 240  
 Asn Ser Gly Asn Val Glu Arg Phe Gln Thr Leu Lys Thr Ala Trp Gly  
 245 250 255  
 Gln Gln Pro Asp Leu Ala Ala Asn Glu Ala Gln Leu Leu Arg Lys Ile  
 260 265 270  
 Gln Leu Leu Cys Leu Met Glu Met Thr Phe Thr Arg Pro Ala Asn His  
 275 280 285  
 Arg Gln Leu Thr Phe Glu Glu Ile Ala Lys Ser Ala Lys Ile Thr Val  
 290 295 300  
 Asn Glu Val Glu Leu Leu Val Met Lys Ala Leu Ser Val Gly Leu Val  
 305 310 315 320  
 Lys Gly Ser Ile Asp Glu Val Asp Lys Arg Val His Met Thr Trp Val  
 325 330 335  
 Gln Pro Arg Val Leu Asp Leu Gln Gln Ile Lys Gly Met Lys Asp Arg  
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 355 360 365

His Gln Ala His Asp Ile Leu Thr  
370 375

<210> 81  
<211> 1257  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (1201)

<220>  
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<222> (1204)

<220>  
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<220>  
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<222> (1217)

<400> 81  
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<210> 82  
<211> 102  
<212> PRT  
<213> Homo sapiens

<400> 82  
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1 5 10 15

Phe Leu Asp Val Arg Met Arg Pro Thr Gly Phe Ser Thr Gly Ser Ala  
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 Leu Trp Asn Phe Gln Ala Glu Ala Gly Glu Gly Asn Gly Ala Ala Trp  
                   35                                  40                                  45  
 Leu Gln Glu Ser Ser Ser Val Pro Glu Pro Gly Ala Arg Cys Gly Ser  
                   50                                  55                                  60  
 Cys Gly Leu Leu Leu Leu Pro Ala Arg Ser Arg Cys Lys Arg Pro Ala  
                   65                                  70                                  75                                  80  
 Glu Cys Trp Gly Trp Ala Arg Thr Ser Gln Cys His Glu Ala Ser Cys  
                                   85                                  90                                  95  
 Ser Phe Glu Phe His Leu  
                                   100

&lt;210&gt; 83

&lt;211&gt; 2520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 83

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<210> 84

<211> 366

<212> PRT

<213> Homo sapiens

<400> 84

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 Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn Glu Arg His  
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 Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr Pro Arg Leu Ala  
 50 55 60  
 Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser Arg Leu Leu  
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 Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr Phe Thr Val  
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 Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu Gln Asp Pro  
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 145 150 155 160  
 Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr  
 165 170 175  
 Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn  
 180 185 190  
 His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val  
 195 200 205  
 Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro  
 210 215 220  
 Gly Leu Leu Ala Thr Arg Val Glu Val Pro Leu Leu Gly Ile Val Val  
 225 230 235 240

Ala Ala Gly Leu Ala Leu Gly Thr Leu Val Gly Phe Ser Thr Leu Val  
 245 250 255

Ala Cys Leu Val Cys Arg Lys Glu Lys Lys Thr Lys Gly Pro Ser Arg  
 260 265 270

His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu Lys Leu Asn Asn  
 275 280 285

Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro Ser Asn Leu Gln Leu  
 290 295 300

Asn Asp Leu Thr Pro Asp Ser Arg Ala Val Lys Pro Ala Asp Arg Gln  
 305 310 315 320

Met Ala Gln Asn Asn Ser Arg Pro Glu Leu Leu Asp Pro Glu Pro Gly  
 325 330 335

Gly Leu Leu Thr Ser Gln Gly Phe Ile Arg Leu Pro Val Leu Gly Tyr  
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Ile Tyr Arg Val Ser Ser Val Ser Ser Asp Glu Ile Trp Leu  
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<210> 85  
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 <212> DNA  
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<220>  
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<220>  
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<210> 86  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> (162)

<220>  
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 35 40 45  
 Val Met Leu Gly Met Thr Leu Ser Ile Val Cys Lys Ser His Phe Phe  
 50 55 60  
 Leu Val Phe Gln Gln Gln Leu His Arg Val Gly Leu Leu Leu Pro Met  
 65 70 75 80  
 Lys Ala Thr Leu Ser Leu Ser Thr Ser Ser Val Trp His Tyr Cys Lys  
 85 90 95  
 Leu Cys Cys Val Val Met Ala Ile Tyr Pro Thr Val Leu Ser Ser Val  
 100 105 110  
 Trp Gly Ser Ala Ala Ser Phe Tyr Val Ile Phe Ile Thr Thr Cys Leu  
 115 120 125  
 Cys Ala Ser Gly Gly Lys Ala Glu Ser Ala Ser Leu Pro Ser Ala Gly  
 130 135 140  
 Leu Thr Met Thr His Tyr Lys Gly Arg Lys Ser Tyr Arg Cys Gln Lys  
 145 150 155 160  
 Met Xaa Gly Lys Trp Thr Val Ile Asn Thr Lys Gln Gln Val Val Ser  
 165 170 175

Ile Lys Glu Lys Asn Ser Met Leu Val Arg Glu Xaa Cys Gln Ser Trp  
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Leu Lys Arg  
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<210> 87  
 <211> 802  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
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<210> 88  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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 Ile Asn His Val Val Val Phe Met Leu Gly Thr Ile Pro Phe Pro Glu  
 35 40 45  
 Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro Asp Ser Asn Gly Met  
 50 55 60  
 Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn Gly Lys Pro Ser Ala  
 65 70 75 80  
 Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu Gly Ser Gln His Pro  
 85 90 95  
 Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser Val Ala Gln Ile Gly  
 100 105 110  
 Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln Gln Thr Pro Val Gly  
 115 120 125  
 Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr Gln Phe Thr Gln Lys  
 130 135 140



Val Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser Phe Ala Val Ser Gln  
 145 150 155 160

Ala Pro Met Thr Pro Ser Pro Ser Glu Met Phe Ile Pro Ala Asn Val  
 165 170 175

Val Leu Lys Trp Tyr Glu Asn Phe Gln Gly Arg Leu Ala Pro Asn Pro  
 180 185 190

Leu Phe Trp Glu Thr  
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<210> 89

<211> 732

<212> DNA

<213> Homo sapiens

<400> 89

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<210> 90

<211> 92

<212> PRT

<213> Homo sapiens

<400> 90

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Leu Thr Gly Leu Val Leu Ser Leu Tyr Ala Leu His Val Lys Ala Ala  
 20 25 30

Arg Ala Arg Asp Arg Asp Tyr Arg Ala Leu Cys Asp Val Gly Thr Ala  
 35 40 45

Ile Ser Cys Ser Arg Val Phe Ser Ser Arg Leu Pro Ala Asp Thr Leu  
 50 55 60

Gly Leu Cys Pro Asp Ala Ala Glu Leu Pro Gly Val Ser Arg Trp Phe  
 65 70 75 80

Cys Leu Pro Gly Leu Asp Pro Val Leu Arg Ala Leu  
 85 90

<210> 91

<211> 901  
 <212> DNA  
 <213> Homo sapiens

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 a 901

<210> 92  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 92  
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 Leu Cys Ser Gln Val Leu Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr  
 35 40 45  
 Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp  
 50 55 60  
 Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu Ser Ser Ala Ala  
 65 70 75 80  
 Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu  
 85 90 95  
 Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu  
 100 105 110  
 Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys Ser Leu Arg Met  
 115 120 125  
 Asn Arg Leu Ala Gly Val Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser  
 130 135 140  
 Ser Leu Leu Gln Ser Val Glu Glu Pro Met Val His Leu Arg Leu Glu  
 145 150 155 160  
 Val Ala Ala Ala Pro Gly Thr Pro Ala Gln Pro Val Ala Met Ser Leu  
 165 170 175

Ser Ala Asp Lys Phe Gln Val Leu Leu Ala Glu Leu Lys Gln Ala Gln  
 180 185 190

Thr Leu Met Ser Ser Leu Gly  
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<210> 93  
 <211> 1579  
 <212> DNA  
 <213> Homo sapiens

<400> 93  
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<210> 94  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 94  
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 Asp Phe Gly Tyr Ser Leu Met Lys Ile Trp Ser Phe Val Phe Leu Pro  
 35 40 45  
 Ala Met Trp Cys Ala Glu Met Leu His Ile Leu Phe Met Gly Leu Arg  
 50 55 60

Val Asn Leu Asn His Glu Thr Phe Leu Ile Ile Cys Cys Glu Ile Tyr  
65 70 75 80

Gln Ala Trp Met Ile Ser Val Phe Leu Val Val Cys Cys Phe Phe Lys  
85 90 95

Glu Val Ile Gln Val Pro Leu Leu Ser Cys Gln His Thr Lys Leu Leu  
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Lys Lys Leu Thr Ile Ser Phe Arg Ser Asn Ser Gln Pro Val Glu  
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<210> 95

<211> 1891

<212> DNA

<213> Homo sapiens

<400> 95

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<210> 96

<211> 287

<212> PRT

<213> Homo sapiens

<400> 96

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 Leu Gly Thr Ala Arg Glu Gly Ala Gly Ala Trp Glu Ala Asp Gln Gly  
                   35                  40                  45  
 Trp Thr Lys Pro His Glu Gly Gly Glu Leu Glu Glu Lys Ser Leu Gly  
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 Asp Leu Trp Gly Lys Glu Leu Arg Ser Pro Ala Ala Pro Gly Glu Thr  
                   65                  70                  75                  80  
 Cys Leu Gln Trp Met Pro Leu Leu Gly Leu Trp Thr Ala Asp Ala Phe  
                   85                  90                  95  
 Phe Leu Leu Asp Thr Trp Leu Leu Gly Leu Gln Val Lys Arg Glu Ser  
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 Gln Pro Ser Leu Phe Pro Ser Val Leu Leu Cys Ser Cys Cys Phe Phe  
                   115                  120                  125  
 Gln Gln Pro Leu Leu Gly Gly Ser Arg Pro Gln Pro Gln Gly Ser Asp  
                   130                  135                  140  
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                   180                  185                  190  
 Ser Pro Ser Phe Gly Cys Ser Leu Arg Cys Val Leu Gly Ser Ser Glu  
                   195                  200                  205  
 Pro Glu Ala Ser Phe Trp Lys Pro Ala Val Leu Pro Ala Pro Val Gln  
                   210                  215                  220  
 Lys Pro Leu Ser Pro Ala Phe Pro Gln Ala Gly Val Gly Val Gly Gly  
                   225                  230                  235                  240  
 Leu Cys Pro Ser Ser Leu Thr Leu Glu Arg Trp Glu Ala Gly Asn Leu  
                   245                  250                  255  
 His Leu Gly Ala Trp Ala Pro Pro Leu Cys Ala Ser Gly Phe Pro Ala  
                   260                  265                  270  
 Pro Gly Arg Gly Cys Ser Pro Ser Trp Thr Pro Ala Cys Pro Ser  
                   275                  280                  285

&lt;210&gt; 97

&lt;211&gt; 2192

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (891)

&lt;400&gt; 97

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&lt;210&gt; 98

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

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Met Leu Ser Val His His Ser Val Leu Ala Met Asp Val Phe Leu Glu
  1                      5                      10                      15

Ile Pro His Ser Pro Leu His Thr Glu Ser Asn Val Lys Asn Leu Leu
          20                      25                      30

Pro Thr Gly Thr Trp Phe Ser Gln Leu Leu Ser Gly Ala Leu Gly Pro
          35                      40                      45

Val Arg Ala Thr Cys Pro Arg Phe Arg Ile Gln His Ile Thr Ser Ala
          50                      55                      60

Pro Pro Leu Pro Ala Ala Phe Leu Ser Tyr Leu Ser Ser Leu Phe Ser

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65	70	75	80
Val Pro Ser His Ile Pro His Ser Cys Pro Gln Thr Leu Gly Leu Glu			
	85	90	95
Gly Pro Gly Leu Leu Pro Arg Pro Pro Leu Leu Ser Leu Ala Tyr Leu			
	100	105	110
Ser Pro Leu Cys Pro Pro Leu Pro Ala His Leu Trp Pro Ala Gln Ala			
	115	120	125
Trp Glu Glu Leu Trp Leu Phe Phe Leu Arg Lys Ser Leu			
	130	135	140

&lt;210&gt; 99

&lt;211&gt; 1774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 99

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&lt;210&gt; 100

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 100

Met Leu Leu Ser Arg Gly Pro Val Leu Gly Gly Leu Ser Glu Asp Ser
1 5 10 15

Phe Ser Cys Leu Cys Lys Ala Val Thr Phe Ser Ala Pro Ser Ser Cys  
                     20                    25                    30  
 Val Asn Phe Thr Val Phe Pro Ser Tyr Ile Leu Ile Pro Pro Ser Pro  
                     35                    40                    45  
 Phe Ser Arg Phe Ser Cys Tyr Ser Ser Ser Ser Pro Leu Val Phe Leu  
                     50                    55                    60  
 Ser Cys Pro Lys Ser Ser Leu Ser Arg Pro Thr Ile Gly Ser Ala Cys  
                     65                    70                    75                    80  
 Pro Val Gln Asn

<210> 101  
 <211> 1324  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
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 ccgtaggctc agagaaggcc atggaggtgc cgccaccggc accgcggagc tttctctgta 180  
 gagcattgtg cctatttccc cgagtccttg ctgccgaagc tgtgactgcc gattcggaa 240  
 tccttgagga gcgtcagaag cggcttccct acgtcccaga gccctattac ccggaatctg 300  
 gatgggaccg cctccgggag ctgtttggca aagatgaaca gcagagaatt tcaaaggacc 360  
 ttgctaatat ctgtaagacg gcagctacag caggcatcat tggctgggtg tatgggggaa 420  
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 aaaa . 1324

<210> 102  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu  
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 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser  
                     20                    25                    30  
 Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro



35                      40                      45  
 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys  
     50                      55                      60  
 Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys Thr  
     65                      70                      75                      80  
 Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro Ala  
     85                      90                      95  
 Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu Ile  
     100                      105                      110  
 Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala Thr  
     115                      120                      125  
 Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala Val  
     130                      135                      140  
 Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr Arg  
     145                      150                      155                      160  
 Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr Gly  
     165                      170                      175  
 Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly  
     180                      185                      190  
 Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala  
     195                      200                      205  
 Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp  
     210                      215                      220  
 Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu  
     225                      230                      235                      240  
 Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln Glu  
     245                      250                      255  
 Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn Leu  
     260                      265                      270  
 Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp  
     275                      280                      285

&lt;210&gt; 103

&lt;211&gt; 977

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 103

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&lt;210&gt; 104

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

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Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
  1                      5                      10                      15

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
          20                      25                      30

Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys
          35                      40                      45

Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln
          50                      55                      60

Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly
          65                      70                      75                      80

Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile
          85                      90                      95

Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln
          100                      105                      110

Pro Arg Pro Ala Phe Thr Ala Ile Arg Arg Asn Pro Pro Met Gly Gly
          115                      120                      125

Asn Val Val Ile Phe Asp Thr Val Ile Thr Asn Gln Glu Glu Pro Tyr
          130                      135                      140

Gln Asn His Ser Gly Arg Phe Val Cys Thr Val Pro Gly Tyr Tyr Tyr
          145                      150                      155                      160

Phe Thr Phe Gln Val Leu Ser Gln Trp Glu Ile Cys Leu Ser Ile Val
          165                      170                      175

Ser Ser Ser Arg Gly Gln Val Arg Arg Ser Leu Gly Phe Cys Asp Thr
          180                      185                      190

Thr Asn Lys Gly Leu Phe Gln Val Val Ser Gly Gly Met Val Leu Gln
          195                      200                      205

Leu Gln Gln Gly Asp Gln Val Trp Val Glu Lys Asp Pro Lys Lys Gly
          210                      215                      220

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His Ile Tyr Gln Gly Ser Glu Ala Asp Ser Val Phe Ser Gly Phe Leu  
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Ile Phe Pro Ser Ala  
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<210> 105  
 <211> 1034  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (618)

<220>  
 <221> unsure  
 <222> (905..906)

<400> 105  
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<210> 106  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (82)

<400> 106  
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 Val Glu Leu Thr Ser Gly Pro Gln Ser Pro Ala Gly Leu Ser Val Arg  
 35 40 45  
 His Ala Arg Val Val Glu Met Gly Pro Pro Gly Pro Leu Ala Val His

50                      55                      60  
 Trp Ala Glu Thr Ser Gly Lys Pro Ala Ala Gly Ala Leu Ser Gly Pro  
 65                      70                      75                      80  
 Leu Xaa Pro Ala Gln Cys Ser Gln Pro Ser Pro Ser Gly Lys Gln Ser  
                     85                      90                      95  
 Val Gln Gln Met Leu Cys Glu Ile Leu Gly Phe Ser Leu Phe Leu Phe  
                     100                      105                      110  
 Cys Phe Val Phe Glu Arg  
                     115

<210> 107  
 <211> 882  
 <212> DNA  
 <213> Homo sapiens

<400> 107  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 882

<210> 108  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 108  
 Met Arg Met Thr Leu Cys Glu Gly Trp Asn Ser Gly Leu Gln Gly Glu  
   1                      5                      10                      15  
 Lys Gly Arg Leu Asp Cys Thr Leu Met Pro Pro Glu Glu Ala Asp Pro  
                     20                      25                      30  
 Leu Leu Arg Trp Ala Trp Ala Arg Pro Ser Leu Ile Gln Val Ala Leu  
                     35                      40                      45  
 Ser Thr Ser Pro Phe Leu Ala Pro Thr Pro Leu Leu Cys Leu Pro Gly  
                     50                      55                      60  
 Ala Leu Pro Val Leu His Leu Pro Pro Gln Lys Glu Ala Ser Phe Ser  
                     65                      70                      75                      80  
 Val Ser Leu Gly Glu Gly Ala Gly Arg Trp Leu Thr Pro Phe Ser Ile  
                     85                      90                      95

Ser Arg Pro Cys His Gly Val Ser Ser Cys Cys Tyr Leu  
100 105

<210> 109  
<211> 1547  
<212> DNA  
<213> Homo sapiens

<400> 109  
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<211> 73  
<212> PRT  
<213> Homo sapiens

<400> 110  
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20 25 30  
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35 40 45  
Pro Ala Ala Val Ser Ala Asp Gly Gln Ala Asn Phe Ser His Val Val  
50 55 60  
Leu Thr Gln Gly Pro Gly Trp Ala Phe  
65 70

<210> 111  
 <211> 650  
 <212> DNA  
 <213> Homo sapiens

<400> 111  
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 gtatcagaat gataatgtag aaacatatat aagccccaga ctgcccccta cagcaaatg 240  
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 tctgtctgaa atgtcttgaa accagggatg ttcttataat aatacttact gtgcagttag 600  
 tggatagcca caagtaatcc ataattttac tttttaaaaa aaaaaaaaaa 650

<210> 112  
 <211> 53  
 <212> PRT  
 <213> Homo sapiens

<400> 112  
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 Ser Pro Ile Lys Cys Leu Phe Val Asn Ile Leu Ile Gly Ser Val Phe  
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 Leu Trp Phe Cys Lys Leu Cys Thr Phe Thr Lys His Trp Leu Phe Ser  
 35 40 45  
 Gly Ser Phe Gln Val  
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<210> 113  
 <211> 1136  
 <212> DNA  
 <213> Homo sapiens

<400> 113  
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<210> 114

<211> 239

<212> PRT

<213> Homo sapiens

<400> 114

Met Ala Tyr Gln Ser Leu Arg Leu Glu Tyr Leu Gln Ile Pro Pro Val  
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Ser Arg Ala Tyr Thr Thr Ala Cys Val Leu Thr Thr Ala Ala Val Gln  
 20 25 30

Leu Glu Leu Ile Thr Pro Phe Gln Leu Tyr Phe Asn Pro Glu Leu Ile  
 35 40 45

Phe Lys His Phe Gln Ile Trp Arg Leu Ile Thr Asn Phe Leu Phe Phe  
 50 55 60

Gly Pro Val Gly Phe Asn Phe Leu Phe Asn Met Ile Phe Leu Tyr Arg  
 65 70 75 80

Tyr Cys Arg Met Leu Glu Glu Gly Ser Phe Arg Gly Arg Thr Ala Asp  
 85 90 95

Phe Val Phe Met Phe Leu Phe Gly Gly Phe Leu Met Thr Leu Phe Gly  
 100 105 110

Leu Phe Val Ser Leu Val Phe Leu Gly Gln Ala Phe Thr Ile Met Leu  
 115 120 125

Val Tyr Val Trp Ser Arg Arg Asn Pro Tyr Val Arg Met Asn Phe Phe  
 130 135 140

Gly Leu Leu Asn Phe Gln Ala Pro Phe Leu Pro Trp Val Leu Met Gly  
 145 150 155 160

Phe Ser Leu Leu Leu Gly Asn Ser Ile Ile Val Asp Leu Leu Gly Ile  
 165 170 175

Ala Val Gly His Ile Tyr Phe Phe Leu Glu Asp Val Phe Pro Asn Gln  
 180 185 190

Pro Gly Gly Ile Arg Ile Leu Lys Thr Pro Ser Ile Leu Lys Ala Ile  
 195 200 205

Phe Asp Thr Pro Asp Glu Asp Pro Asn Tyr Asn Pro Leu Pro Glu Glu  
 210 215 220

Arg Pro Gly Gly Phe Ala Trp Gly Glu Gly Gln Arg Leu Gly Gly  
 225 230 235

<210> 115

<211> 1617

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1164)

&lt;400&gt; 115

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&lt;210&gt; 116

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

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Met Leu Glu Arg Ala Pro Ser Ile Arg Gly Leu Thr Leu Ala Asp Ser
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Val Pro Ser Leu His Cys Cys Leu Pro Ala Asp Phe Leu Asn Cys Ser
          20             25             30

Cys Ala Ile Asp Asn Val Leu Thr Cys Phe Ser Leu Phe Val Asn Val
          35             40             45

Phe Ala Leu Gln Ala Ala Phe Leu Pro Tyr Cys Ile Glu Lys Glu Lys
          50             55             60

Arg Leu Gly Leu Leu Leu His Ile Leu Ser Phe Tyr Thr Phe Ile Phe
          65             70             75             80

Leu Glu Trp Ser Asp Ser Glu Leu Asp Ser Gln Asn His Arg Ser Ala
          85             90             95

Val Lys Gly Phe
          100

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<210> 117  
 <211> 849  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
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 tgtgtgcttg ttaaggctcc aaaccacct ctctttccca ggctgggtcc ctacaccccc 240  
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<210> 118  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 118  
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 20 25 30  
 Gln Leu Pro Glu Ala Val Cys Leu Leu Arg Leu Gln Thr His Leu Ser  
 35 40 45  
 Phe Pro Gly Trp Val Pro His Thr Pro Pro Leu Leu Met Tyr His His  
 50 55 60  
 Leu Leu Pro Ser Thr Ser Pro Val Cys Ser Pro Leu Pro Arg Ser Thr  
 65 70 75 80  
 Leu Leu Ala Leu Phe Pro Thr Cys Leu Pro Ile Pro Thr Ser Phe Lys  
 85 90 95  
 Ser Leu

<210> 119  
 <211> 925  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (883)

&lt;400&gt; 119

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aaaaaaaaa aaaaaaaaaa aaaaa 925

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&lt;210&gt; 120

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

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Met Val Lys Leu Gly Cys Ser Phe Ser Gly Lys Pro Gly Lys Asp Pro
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Gly Asp Gln Asp Gly Ala Ala Met Asp Ser Val Pro Leu Ile Ser Pro
  20             25             30

Leu Asp Ile Ser Gln Leu Gln Pro Pro Leu Pro Asp Gln Val Val Ile
  35             40             45

Lys Thr Gln Thr Glu Tyr Gln Leu Ser Ser Pro Asp Gln Gln Asn Phe
  50             55             60

Pro Asp Leu Glu Gly Gln Arg Leu Asn Cys Ser His Pro Glu Glu Gly
  65             70             75             80

Arg Arg Leu Pro Thr Ala Arg Met Ile Ala Phe Ala Met Ala Leu Leu
  85             90             95

Gly Cys Val Leu Ile Met Tyr Lys Ala Ile Trp Tyr Asp Gln Phe Thr
 100             105             110

Cys Pro Asp Gly Phe Leu Leu Arg His Lys Ile Cys Thr Pro Leu Thr
 115             120             125

Leu Glu Met Tyr Tyr Thr Glu Met Asp Pro Glu Arg His Arg Ser Ile
 130             135             140

Leu Ala Ala Ile Gly Ala Tyr Pro Leu Ser Arg Lys His Gly Thr Glu
 145             150             155             160

Thr Pro Ala Ala Trp Gly Asp Gly Tyr Arg Ala Ala Lys Glu Glu Arg
 165             170             175

Lys Gly Pro Thr Gln Ala Gly Ala Ala Ala Ala Thr Glu Pro Pro
 180             185             190

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Gly Lys Pro Ser Ala Lys Ala Glu Lys Glu Ala Ala Arg Lys Ala Ala  
 195 200 205

Gly Ser Ala Ala Pro Pro Pro Ala Gln  
 210 215

<210> 121  
 <211> 1645  
 <212> DNA  
 <213> Homo sapiens

<400> 121  
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<210> 122  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 122  
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 Thr Pro Leu Cys Gln Ser Lys Met Cys Glu His Ile Pro Glu Ala Ser  
 20 25 30  
 Lys Pro Ala Ala Ser Gly Ile Ile Thr Ile Met Val Ala Gly Ala Arg  
 35 40 45  
 Gly Ala Ile Cys Gln Gln Gly Glu Lys Tyr Ala His Leu Arg Val Gly  
 50 55 60

Val Leu Glu Lys His Arg His Gly Ala Asp Ser Gln Val Gly Trp Gln  
 65 70 75 80

Glu Ser Pro Gly Val Arg Arg Gly Arg Cys Ser Arg Gln Lys Lys Pro  
 85 90 95

Gln Gln Gln Arg Cys Gly Gly Gly Arg Ile Arg Ala Leu Leu Arg Glu  
 100 105 110

Cys Ile Val Gly Ala Ser Val Gln Glu Arg Ala Leu Arg Asp Glu Val  
 115 120 125

Arg Gly Pro Arg Gly Ser Gln Pro Gly Ala Cys Lys Ala Ala Arg His  
 130 135 140

Trp Gly Ala Met Glu Gly Ser Ser Arg Arg Glu Ala Cys Ser Gly Trp  
 145 150 155 160

Cys Phe Arg Lys Leu Pro Gln Leu Thr Gly Leu Glu Gly Ser Val  
 165 170 175

<210> 123  
 <211> 2515  
 <212> DNA  
 <213> Homo sapiens

<400> 123  
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 tacaggctgc ctcatctcc tctctgccc ctgcttccac ccacctggaa tcaacttctcc 1800  
 aggtcataca aagcacctt gccccacaca aggatccaag caggctgacc aacagaagtc 1860  
 atcttgagga tcttgtgaaa actatagatt cccatgctct tccccagac cctctgatc 1920

```

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cacacatgca caaatacaaaa tgcatacatg tgtgacacaa atgcatttta gtcatactgt 2160
cactgtgccc aggtctcctt ccgttggttc tacaaataat cattgagtaa acaatcatct 2220
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```

&lt;210&gt; 124

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

```

Met Gly Arg Ser Phe Glu Cys His Thr Pro Gln Phe Ala Thr Lys Pro
  1             5             10             15

```

```

Gln Ala Glu Ser Cys Val His His Thr Arg Gln Lys Ser Val Ser Val
          20             25             30

```

```

Arg Val Leu Ala His Met Ser Pro Leu Cys Pro Pro Leu Tyr Gly Ile
      35             40             45

```

```

Gln Ser Met Phe Val Lys Ala Tyr His Tyr Val Asn Cys Gln Asn Met
      50             55             60

```

```

Val Leu Ser Arg Asn Gly Thr Ala Leu Phe Ile Gln Ser Leu Tyr Arg
      65             70             75             80

```

```

Gly Ser Thr Met His Leu His Leu Ser Lys Ser Asn Tyr
          85             90

```

&lt;210&gt; 125

&lt;211&gt; 1763

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

```

gcctcagcaa caaagaaaaa gtgaattttt aatgctgaag ataaagtaag ctaaagtacc 60
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acagaatcac ttgaaaatgg atgccagtca tctcttggtc ccactactga attcttataa 180
agtgggtggca agatagggaa gggataatct gagaattttt aaaagatgat ttaatgagaa 240
gaagcacaat tttgattgtg atgagtcact ttctgtaaac aatcttggtc tatctttacc 300
cttatacctt atctgtaatt taccatttat tgtatttgca aagcgagtag gggttgaac 360
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tggcatttta caccgctgcg agtattgtta tatctaatac tattttaaaa gatttttggt 540
aatatgaagc ttgaatactg gtaacagtga tgcaatatac gcaagctgca caacctgtat 600
attgtatgca ttgctgcgtg gaggtgtgtt atttcaacct ttttaaaaat tgtgtttttt 660
agtaaaatgg cttatttttt cccaaaagggtg gaatttagca ttttgtaatg atgaatataa 720
aaatacctgt catccccaga tcatttaaaa gttaactaaa gtgagaatga aaaaacaaaa 780
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ggacttaatt cagctgtctg tagtgaataa aagtgggaaa ttttcaaaag tttctcctgc 1680  
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tgaaaaagaa aaaaaaaaaa aaa 1763

<210> 126

<211> 102

<212> PRT

<213> Homo sapiens

<400> 126

Met Trp Ser Asn Pro Ser His Ile Ser Ser Thr Ser Asn Phe Ser Ile  
1 5 10 15

Leu Val Ile Phe Ile Ile Trp Tyr Cys Ile Leu Pro Ser Leu Phe Ile  
20 25 30

Pro Gln Ile Asp Ser Tyr Leu Ser Leu Ile Gln Arg Gly Gln Leu Ser  
35 40 45

Asp Gly Phe Cys Cys Gly Leu Asn Ala Val Pro Val Phe Ser Ser Ser  
50 55 60

Lys Val Asp Leu Gly His Cys Arg His Arg Thr Trp Ile Ala Ser Asp  
65 70 75 80

Gly Leu Leu Tyr His Phe Ser Ser Phe Ser Phe Pro Gly Asp Leu Phe  
85 90 95

Pro Leu Asn Glu Ser Asn  
100

<210> 127

<211> 1698

<212> DNA

<213> Homo sapiens

<400> 127

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attgaagcta gtgtctctca ctttcttagg tgtatcagag agaggaagtg gaaggccagt 180  
agtagcatct tcatacttac ttttgccagc ccagcctcca tttcaaagac tttgtcttcc 240  
atcctatcca atgacatggg cagggatggg ctctgaggag gcagtgaggc cccaccttgg 300  
tttgctccac tgtggtgtgt agtctccaaa cagcttaagg gtttttaagt tttctcacga 360  
ttacctccac tccactcatc tactatcagc atcagaaagg ttaacatccc tgggaccatt 420  
ctacttataa aagagatgaa ctagtgtgct ttctccccct ttccaggtgt gccatccata 480  
tacaatctcc tcttgcccaa gttcaacaaa tgtttccagg gaaccccggt gggtgaggca 540  
aagttagcaa gatgtattga gttaagtttt tctagaggac aaaagtattt cttgtccctt 600  
ttccctcatg ctcatatgtt ttagctgagg cgtaaatggc caagttgagt aatatctgtg 660  
gaactgagac agagagccag ggacccatgt acccagggac cagtcacctg gggaatcaca 720  
cagtggtcca gactagactg ctctatccca ccagaactct gctgctgttc atttccatca 780

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ggaccaccca ggaaagcaaa taagttagcc ttctcatcat taggtcacct aatctcttgg 840
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agggatagaa aatggaataa ccaagaggct gtgtcatttt ttaagaggat ggcaaggatg 960
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cctttcccta ctttactaat gtatccctta tgtggtacca gcaatggagg acaggcagac 1620
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aacaacaaaa aaaaaaaa
1698

```

&lt;210&gt; 128

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

```

Met Cys Leu Arg Lys Ser Arg Ile Phe Gln Val Val Glu Asn Cys Cys
  1             5             10             15

Lys Met Glu Leu Lys Leu Val Ser Leu Thr Phe Leu Gly Val Ser Glu
          20             25             30

Arg Gly Ser Gly Arg Pro Val Val Ala Ser Ser Tyr Leu Leu Leu Pro
      35             40             45

Ala Gln Pro Pro Phe Gln Arg Leu Cys Leu Pro Ser Tyr Pro Met Thr
      50             55             60

Trp Ser Gly Met Gly Ser Glu Glu Ala Val Arg Pro His Leu Gly Leu
      65             70             75             80

Leu His Cys Gly Val
          85

```

&lt;210&gt; 129

&lt;211&gt; 2110

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

```

agcagagaag attgaagatg tggaatcac actggtgtga tgatgggctt gcccattccat 60
tactgtctaca atcaaggcca ggcttgagat ttggccagtc ttgtttttta ggcacctttg 120
catgatgatg actcttgaac agagcaaaaa acaaggagga ttatgtgtga ctgggttgcc 180
tggtagactc ctcccacgtt ttgaatatct cgtgcctttt ttttttgttg tcattttcta 240
tgtcattttct cctaccatag cacaatcct agcggaccct atgatcaaag aggggggcag 300
cctcatgctt aacagtgggc tgttttatat gaagactcaa gaacaagcct cattccagg 360
cacagtcctt aaattactga tcatgtgcac tcgtacagta tattactgtg accacaagg 420
atgtggcaaa gattctcatc tttcttcaag tggcttttgc tcatctgatt gagaattaat 480
cagatcatgt tggctacata aggaacaga aggagggatt tcaggagagg ctggctcctc 540
cccaaggtta gtccccagac tgagaaagt aaaccttatt gggaaaaatt ggactgcct 600
gaatttagca ccaattgcat taacgcacat ctcttcaca actaacagac ttaaaataac 660
agtgtccttc gtattaatat ctgtgccatt catttagaat tagcagagct aatatggagg 720

```

```

ggctgaacta gtagccacat cttgttcac acatagacta atagaaagga gctgtggcta 780
aagcagaaat ggaacttccg gatctgaaat tagcccatat aatgttcttt tgtatttggg 840
tatttttcat cttaatTTTT acagcatata ctcttcttac cagtatcctt agaatccaaa 900
tgtctagata agttgaggac acatactgc attgttgagc ttctctactg gggacgcccc 960
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gaccaactgc tatggtggaa aatgcagctt ccagggtcca ctaccctgac atttccgtgg 1080
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agtttgatt tactatgtat aaaatgttga ataataaaaa aaatggaatt aaaaaaaaaa 2100
aaaaaaaaa 2110

```

&lt;210&gt; 130

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

```

Met Met Met Thr Leu Glu Gln Ser Lys Lys Gln Gly Gly Leu Cys Val
  1             5             10             15

Thr Gly Trp Pro Gly Arg Leu Leu Pro Arg Phe Glu Tyr Phe Val Pro
      20             25             30

Phe Phe Phe Val Val Ile Phe Tyr Val Ile Ser Pro Thr Ile Ala Gln
      35             40             45

Ile Leu Ala Asp Pro Met Ile Lys Glu Gly Gly Ser Leu Met Pro Asn
      50             55             60

Ser Gly Leu Phe Tyr Met Lys Thr Gln Glu Gln Ala Ser Phe Gln Gly
      65             70             75             80

Thr Val Pro Lys Leu Leu Ile Met Cys Thr Arg Thr Val Tyr Tyr Cys
      85             90             95

Asp His Lys Gly Cys Gly Lys Asp Ser His Leu Ser Ser Ser Gly Phe
      100             105             110

Cys Ser Ser Asp
      115

```

&lt;210&gt; 131

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 131

```

ccccgtgtttc cccgggctggg tatttgccctc gcacccatggc gcccaagggc aaagtgggca 60
cgagaggggaa gaagcagata tttgaagaga acagagagac tctgaagttc tacctgcgga 120
tcatactggg ggccaatgcc atttactgcc ttgtgacgtt ggtcttcttt tactcatctg 180
cctcattttg ggccctgggtg gccctgggct ttagtctggc agtgtatggg gccagctacc 240
actctatgag ctccgatggca cgagcagcgt tctctgagga tggggccctg atggatgggtg 300
gcatggacct caacatggag cagggcattg cagagcacct taaggatgtg atcctactga 360
cagccatcgt gcagggtgctc agctgcttct ctctctatgt ctggtccttc tggcttcttg 420
ctccaggccg ggccttttac ctctgtggg tgaatgtgct gggcccttg ttcactgcag 480
acagtggcac cccagcacca gagcacaatg agaaacggca gcgccgacag gagcggcggc 540
agatgaagcg gttatagcca ttgacattat tgccacaggc cactggccct ggggtggctct 600
gtcagggtgc acagccctc atgctggag caatgagggt ttagtccagg ggccaaaagc 660
agtctgaggt attgggtata cttatactct atagggtcgt tgaataaatg gcttagaatg 720
tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa

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752

&lt;210&gt; 132

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

```

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
  1             5             10             15

Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
      20             25             30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
      35             40             45

Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
      50             55             60

Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
      65             70             75             80

Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
      85             90             95

Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
      100            105            110

Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu
      115            120            125

Ala Pro Gly Arg Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro
      130            135            140

Trp Phe Thr Ala Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys
      145            150            155            160

Arg Gln Arg Arg Gln Glu Arg Arg Gln Met Lys Arg Leu
      165            170

```

&lt;210&gt; 133

&lt;211&gt; 698

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 133

```

ggcagccatg gtcggggcgc tgtgaggctg ctgggtccgc ctggggcggg cccgcccgt 60
catcccgttg ggcccactg tggtagagac ctccatgagc cggccccagg tagccctgct 120
gggcctgagt ctgctgctca tgctcctact gtatgtgggg ctgccaggcc cccctggcaa 180
gacttcctgc ctctggggag accccaatgt cacagtctg gctgggtctca cccctggcaa 240
ctcgcccatc tttaccgag aggtgctccc acccaccag aactacacc aggagcaatt 300
ctgggctgtg aagactccaa cccttatcct gtatggagag ctggaccaca tcctggctcg 360
agagtcaact cgccagctcc gccacctgcc caaccactct gtggtgaagc tacgcaatgc 420
aggccatgcc tgttacctcc acaagccgca agacttcac cttgtctgct ttgccttctc 480
tgaccatcta ccttgaacta acccactccc agctcccagc ctggcatgag cttggacagt 540
ctggaccgcc accctccctg aaccaggag acagcctctg ggattggagg ccagaggcca 600
gggtcagacc cagccaggac tcctcatttc atctcacaga cacaataaaa aagcatattt 660
gtcctgccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 698

```

&lt;210&gt; 134

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

```

Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu Gly Gly Ala Arg
  1             5             10             15

Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr Ser Met Ser Arg
      20             25             30

Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu Met Leu Leu Leu
      35             40             45

Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser Cys Leu Trp Gly
      50             55             60

Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro Gly Asn Ser Pro
      65             70             75             80

Ile Phe Tyr Arg Glu Val Leu Pro Pro Thr Gln Asn Tyr Thr Gln Glu
      85             90             95

Gln Phe Trp Ala Val Lys Thr Pro Thr Leu Ile Leu Tyr Gly Glu Leu
      100            105            110

Asp His Ile Leu Ala Arg Glu Ser Leu Arg Gln Leu Arg His Leu Pro
      115            120            125

Asn His Ser Val Val Lys Leu Arg Asn Ala Gly His Ala Cys Tyr Leu
      130            135            140

His Lys Pro Gln Asp Phe His Leu Val Leu Leu Ala Phe Leu Asp His
      145            150            155            160

Leu Pro

```

&lt;210&gt; 135

&lt;211&gt; 1825

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 135

```

tgtgcggttat gtaggttgta atgaagctaa cagtttcagt tatgtactac tatttttgtc 60
catacttagt tcattgtaaa ctctatatta atttctttga taacatgtat ttgatttttt 120
tgcaatacgg ctttcaggtt cttgccattc ttcagattct catgcttatt cagattttctc 180
atttggctgg cattttgtta tcagtgaacc aaaattatct ctttttaa atacataaga 240
caaaagcacc agtagtcagt attctagttc tccttactaa tttacggagg tgtgatctgg 300
gtgattttta aattaattta attatcattt catattcata gtgatgattt ttaaaatttt 360
acaaactttt cacctatata aacatcttta ttgtcaggtg tctgacaagc taatttcttt 420
gctaactatt ttagttatta atatattatg taggttgat cagaattttg tttttcacc 480
aatgcttttt cacaattccc aagtcaagaa ggatgcatta caatgtttac attagcatct 540
aaaggcaatg taaagtcggg aaacattttt agtatataat ttcataattc aaagacattt 600
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aatcaatttt gactgtacaa tctagttagt tttgacagct gtataaagca gtttcccacc 1800
accacgaaaa aaaaaaaaaa aaaaaa
1825

```

&lt;210&gt; 136

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

```

Met Lys Leu Thr Val Ser Val Met Tyr Tyr Tyr Phe Cys Pro Tyr Leu
  1              5              10              15

Val His Cys Lys Leu Tyr Ile Asn Phe Phe Asp Asn Met Tyr Leu Ile
      20              25              30

Phe Leu Gln Tyr Gly Phe Gln Val Leu Ala Ile Leu Gln Ile Leu Met
      35              40              45

Leu Ile Gln Ile Ser His Leu Ala Gly Ile Leu Leu Ser Val Asn Gln
      50              55              60

Asn Tyr Leu Ile Leu Asn Ser His Lys Thr Lys Ala Pro Val Val Ser
      65              70              75              80

Ile Leu Val Leu Leu Thr Asn Leu Arg Arg Cys Asp Leu Gly Asp Phe
      85              90              95

```

&lt;210&gt; 137

&lt;211&gt; 1503

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (1193)

<400> 137

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aaa

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<210> 138  
<211> 174  
<212> PRT  
<213> Homo sapiens

<400> 138

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Met Val Ser Gln Phe Leu Asp Glu Cys Asn Met Met Met Val Met Met
  1              5              10              15

Thr Met Ser Leu Ile Ile Val His Leu Leu Pro Leu Gly Leu Arg Glu
      20              25              30

Arg Glu Gly Leu Phe Phe Phe Leu Pro Ile Phe Pro His Ser Val Phe
      35              40              45

Leu Leu Val Thr Tyr Thr Thr Cys Asn Asp Ala Met Thr Asn Ser Ala
      50              55              60

Pro Lys Pro Leu Tyr Leu Gly Leu His Phe Arg Leu Met Cys Pro Asp
      65              70              75              80

Leu His Ala Leu Leu Ala Phe Phe Trp Tyr Leu Asn Val Gly Ser Leu
      85              90              95

Phe Gln Glu Phe Asn Ile Asn Phe Gln Lys Tyr His Gly Thr Cys Asp

```

<400> 140  
Met Thr Phe Ser Ser Tyr Lys His Cys Pro Leu Thr Pro Cys Cys Ser  
1 5 10 15

Val Gly Val Asp Cys Arg Asn Ala Pro Leu Thr Ala Asn Thr Lys Val  
 20 25 30

Gly Ser Val Gln Ser Leu Leu Tyr Gln Ser Lys Ala Asp Asn Ile Ala  
 35 40 45

His Thr Cys Leu Val Leu Leu Gly Cys Cys His Thr Val Gln Lys Trp  
 50 55 60

Ala Leu Tyr Leu Val Glu Ala Leu Leu Trp Gly Ser Leu Asn Gln Asp  
 65 70 75 80

Ala Ala Thr Met Lys Ala Leu Lys Val Thr  
 85 90

<210> 141  
 <211> 1067  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 tggaatggta actatttttt cccatcgctt ttttgagaga aggaagtgtg atgactgatg 180  
 atcttgaaaa gccatttctt gattgcacgt tgactggaat tctttctttg tgtctgtgga 240  
 ctagecatgc tgtttgtaaa atgaagattc gggactggct catatctttt tatctaacta 300  
 gatgtcagat cttgaaatct gtattctcga agcaattctg ccacttgatc gtattcacag 360  
 gggccctggg aggcctcctt agaaggacca tttctgttcc tagagcttaa ctagaattca 420  
 ttcttcactg aaaaaaaaaa aagttaacta agaaagcatt tctttcctaa tctcactcaa 480  
 atctgcagaa ttatttgtaa ttagtaatac aaaatctggc caaaaggaga cttgtaaata 540  
 gcgtaaatg gtgtcttatg ctaaacggtg gaatgtatag gcagagaagc tctttgaagt 600  
 tgtcagatga gctgggctca caagcctgat tcaaacaggc tgtcggcttc ctctcaccct 660  
 ttaatactgt gcagcccaaa ctctaggac tcttgaacat ctgagcagtt ttgtgctttg 720  
 agccactttt tgacaaaaat ggctccattt ttccacagcg tggttttctt aaaatagttt 780  
 aatgttttat agtctcatag tagtagtgtt gctttctaag ctataaccgt cgactttatt 840  
 cttctactct gaaaaatctt tacttgtttg agtggtttta atttttataa agggagcctt 900  
 aatggattgg ttttcataat ttaatatctt ttgtatttgc tcttgataaa ttgtttttta 960  
 cggaaagtat taaagaattg agggtggaat tcttagaacc aaagttattc ttaataaaaa 1020  
 tcaccacatg cttggacca aaaaaaaaaa aaaaaaaaaa aaaaaaa 1067

<210> 142  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

<400> 142  
 Met Thr Asp Asp Leu Glu Lys Pro Ile Ser Asp Cys Thr Leu Thr Gly  
 1 5 10 15

Ile Leu Ser Leu Cys Leu Trp Thr Ser Asp Ala Val Cys Lys Met Lys  
 20 25 30

Ile Arg Asp Trp Leu Ile Ser Phe Tyr Leu Thr Arg Cys Gln Ile Leu  
 35 40 45

Lys Ser Val Phe Ser Lys Gln Phe Cys His Leu Ile Val Phe Thr Gly  
 50 55 60

Ala Leu Val Gly Ser Phe Arg Arg Thr Ile Ser Val Pro Arg Ala  
 65 70 75

<210> 143  
 <211> 1415  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (1208)

<400> 143  
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 tggcctctac ctgcctcaca ggactgctc atcccaccta ggcatggctg gatacttgag 180  
 ccatgctcca gccatgttgg cttctttcag ttctctcagt gcccttggct tcttctgccc 240  
 acaggggtctt tgcataactt ttccacttg caagtctatt ctcttttctt tcaacctctt 300  
 cccatttgc ctaattaact tctctagatc ctctacatct cagtccaac ttttcttgc 360  
 accagtcaca ttcgtgacc tctgtgacca ggccaacccc gtaccaaaaa tattcttccg 420  
 ccaagcattt ccagttatca ccttgcatth ctctcttga tgtttttgat ttatgtctac 480  
 atccccacc taaccgtaag ctcttagatg aaaaagactt gttctcttta acctgctcat 540  
 tattccctca gcacctcaa gtatagttgg cccatcacac agcagggtgct taataaatat 600  
 ttgatgattt ctttaagtga tgagtgaatg aacctgttga ttctattcac cttagtctcc 660  
 ctcaaattht ttcaaaaaga gttactaata gtgtgaaagc tctctgatg aagaatgcca 720  
 ctctgtagtt ttaactcagt aagtaagaaa gaatcataaa actcaactag gccattgaca 780  
 aaatgaaagt acagtcaatg accaaaatcg tcccttttta atttttcttc taggaattta 840  
 agaaaagaag gcaaattag caccagtggc cctgtgaagt gagccctagg ccatatctgg 900  
 atgcttttta ttttaggatc atttccaaac tagttacaat gatttttatt tgataaagtg 960  
 aaattcatcc caatctctag agggatactc agtctctaaa tgtttcaatg gtgccatcat 1020  
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 aggtttgaat ttttgtgtaa tttttatatt tagtttaact ttctgtttta aaaaggaagt 1140  
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 atgagggngt gtggggagctt ggtatcattt agtgttttat gagcaataac atgaatggta 1260  
 agataatttt aggaagtggg agacagattg gattcacttg gaacacagcc agaaaaatca 1320  
 ataaatgatt atttactaat tcagaaaaga tgatgattct aagtctttta aaatgcattt 1380  
 ttaaaaactg ttttccagtt cggcaaaaaa aaaaa 1415

<210> 144  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Ala Gly Tyr Leu Ser His Ala Pro Ala Met Leu Ala Ser Phe Ser  
 1 5 10 15  
 Ser Ser Ser Ala Pro Cys Phe Phe Leu Pro Gln Gly Leu Cys Ile Thr  
 20 25 30  
 Phe Ser Thr Cys Lys Ser Ile Leu Phe Ser Phe Asn Leu Phe Pro Ile  
 35 40 45  
 Cys Leu Ile Asn Phe Ser Arg Ser Ser Thr Ser Gln Phe Lys Leu Phe  
 50 55 60  
 Phe Ala Pro Val Thr Phe Ala Asp Leu Cys Asp Gln Ala Asn Pro Val  
 65 70 75 80

Pro Lys Ile Phe Phe Arg Gln Ala Phe Pro Val Ile Thr Leu His Phe  
85 90 95

Phe Leu

<210> 145

<211> 1118

<212> DNA

<213> Homo sapiens

<400> 145

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tctggaattc tgagtgtgc aaccttgcaa ctttggtcca gttagaattg gatcggaagc 180
tagtcaggca gcaggcgagc cccagttact cccagataac ctctgcatt gctgtggttt 240
ctggagcttt ctgtagggtg ggcagtggga gccagggtag gtggggtagg cccgcccctg 300
cgagtgtctt cggcaccctc ccttcacccc cgccctgcgc gcggtgctct gcgccgacag 360
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tctgtctcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1118

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<210> 146

<211> 143

<212> PRT

<213> Homo sapiens

<400> 146

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Met Leu Gln Thr Leu Glu Lys Asp Pro Gly Gln Arg Pro Leu Leu Phe
  1             5             10            15

Ile Trp Asn Ser Glu Cys Cys Asn Leu Ala Thr Leu Val Gln Leu Glu
      20             25             30

Leu Asp Arg Lys Leu Val Arg Gln Gln Ala Ser Pro Ser Tyr Ser Gln
      35             40             45

Ile Thr Ser Cys Ile Ala Val Val Ser Gly Ala Phe Cys Arg Val Gly
      50             55             60

Ser Gly Ser Gln Gly Arg Trp Gly Arg Pro Ala Pro Ala Ser Val Phe
      65             70             75            80

Gly Thr Leu Pro Ser Thr Pro Pro Cys Ala Arg Cys Ser Ala Pro Thr
      85             90            95

Ala Arg Gln Pro Leu Ser Pro Arg Pro Arg Pro Trp Trp Arg Gly Glu
      100            105            110

```



Leu Gly Gly Leu Ser Trp Ser Arg Trp Gln Ser His Ser Trp Ser Pro  
 115 120 125

Ser Trp Gly Gly Ser Arg Ala Cys Ala Pro Asp Ser His Leu Glu  
 130 135 140

<210> 147

<211> 1582

<212> DNA

<213> Homo sapiens

<400> 147

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ggtggctgca ggtggagtct gtggcggtgt gcgcacaccc aggggctccc ccgatgctgg 180
ttactatctg ggctatggtg gccacagctg tcttgccctt cctcacggcc gtgctgggtg 240
ttaccgtggt caccgcgagg gacacggagg ggccaggcag agcagcccta gttcacctca 300
ccgggagccc ccgcccagaag gtgggcacct ctgggagggg gggactgcca ggccttgggg 360
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gcagatttgg ggctgccagg tggcgccagg tccccttggc cagccccagc cgcccccttc 480
ttctgtcccc agggcctcgg cttcacagga tggggctgcc agtgtcctgg gccctcctg 540
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ggcctccccg ggctccagag aaggcccgcg tctaataaaa gcgccagcgc aggatgaaaa 1560
aaaaaaaaaa aaaaaaaaaa aa 1582
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<210> 148

<211> 149

<212> PRT

<213> Homo sapiens

<400> 148

Met Leu Val Thr Ile Trp Ala Met Val Ala Thr Ala Val Leu Pro Leu  
 1 5 10 15

Leu Thr Ala Val Leu Gly Val Thr Val Val Thr Arg Arg Asp Thr Glu  
 20 25 30

Gly Pro Gly Arg Ala Ala Leu Val His Leu Thr Gly Ser Pro Arg Gln  
 35 40 45

Lys Val Gly Thr Ser Gly Arg Glu Gly Leu Pro Gly Leu Gly Ala Ser  
 50 55 60

Cys Ala Glu Ser Glu Leu Glu Arg Glu Thr Gln Glu Pro Arg Ser Cys

```

<400> 150
Met Met Arg Cys Leu His Asn Phe Leu Thr Asp Gly Val Leu Arg Arg
  1              5              10              15

Gly Arg Ser Leu Lys Thr Ser Arg Ala Tyr Gly Gln Arg Trp Arg Pro
      20              25              30

Ser Pro Arg Asn Trp Ser Phe Trp Thr Glu Ser Cys Ala Ser Cys Cys
      35              40              45

```

Trp Arg Ala Trp Arg Gly Cys Cys Gly Thr Ser Trp Pro Cys Glu Pro  
 50 55 60  
 Leu Asp Asp Ala Leu Glu Gln Gly Gln Ser Leu Gly Pro Val Glu Pro  
 65 70 75 80  
 Leu Asp Gly Pro Ala Gly Ala Val Leu Glu Cys Leu Val Leu Ser Ser  
 85 90 95  
 Gly Met Leu Val Pro Glu Leu Ala Ile Pro Val Val Tyr Leu Leu Gly  
 100 105 110  
 Ala Leu Thr Met Leu Ser Glu Thr Gln His Lys Leu Leu Ala Glu Ala  
 115 120 125  
 Leu Glu Ser Gln Thr Leu Leu Gly Pro Leu Glu Leu Val Gly Ser Leu  
 130 135 140  
 Leu Glu Gln Ser Ala Pro Trp Gln Glu Arg Ser Thr Met Ser Leu Pro  
 145 150 155 160  
 Pro Gly Leu Leu Gly Asn Ser Trp Gly Glu Gly Ala Pro Ala Trp Val  
 165 170 175  
 Leu Leu Asp Glu Cys Gly Leu Glu Leu Gly Glu Asp Thr Pro His Val  
 180 185 190  
 Cys Trp Glu Pro Gln Ala Gln Gly Arg Met Cys Ala Leu Tyr Ala Ser  
 195 200 205  
 Leu Ala Leu Leu Ser Gly Leu Ser Gln Glu Pro His  
 210 215 220

<210> 151  
 <211> 1111  
 <212> DNA  
 <213> Homo sapiens

<400> 151  
 attgaattct gccccacatg ttgacagtag agttggaact ggattccttg gattacttat 60  
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 gctattttatt gccacaatg gcctctcttt gtgtccatat atgccttaca ccgtgctgac 180  
 ctgggtatca tccatgtgct ctgaagcatc caactttact ttgcaggtgc atcaatgtag 240  
 tctgtgccct gaactgagta accgtgttcc tgaaaagtac actagggaaa ttcacctgct 300  
 tgcttgctct tgtattggca tggcacttgt gattgcacca tggagcatgc tcagagctat 360  
 taaattggtc tcccatctcc caccaggata tgaaaggccc atatgggagg ccacgtaatc 420  
 acttattaca gtggttacat aatacactgg ctactgcag actctcttgt ttttgatac 480  
 agtttcgtgc tggcttcatt tgccaattgt gttgtttagt tcggaagtaa gagggctctg 540  
 agattgaggg gtagggaggg ctacactgac tgatccgtgg cttaagacag gagattatct 600  
 ctgtactcca gtggcatctc cttagccaag atgtgaaata aaaatcatag ttgcctcat 660  
 ttaaaaattc taataaagca ctcaaaacttt gaaaagcttt tacttttccc tcctactaaa 720  
 aaaaatgtat gtacctcata gccctgtgtc atttagtggt cagcactttt gggaacatca 780  
 gttggtgaac tttaaaattt gctgtctact cactgggcac ggtggctcac acctgtaac 840  
 ccagcacttt gggaggctga ggcaggtgga tcacctgagg tcaggagttt gagaccagcc 900  
 tgaccaacat ggtgaaaccc cgtctctact aaaaatgcag aaattaggtg ggcgcctgta 960  
 atcccagcta cttgggaggc tgaggcgaga taatcgcttg aacctgggag gcagaggttg 1020  
 cagtgaagcc agattgcacc actgtcgccc accctgggtg ataagagtga aactccttct 1080  
 caaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1111

<210> 152  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
 Met Leu Phe Ile Ala Asn Asn Gly Leu Ser Leu Cys Pro Tyr Met Pro  
           1                  5                  10                  15  
 Tyr Thr Val Leu Thr Trp Val Ser Ser Met Cys Ser Glu Ala Ser Asn  
                   20                  25                  30  
 Phe Thr Leu Gln Val His Gln Cys Ser Pro Val Pro Glu Leu Ser Asn  
                   35                  40                  45  
 Arg Val Pro Glu Lys Tyr Thr Arg Glu Ile His Leu Leu Ala Cys Leu  
           50                  55                  60  
 Cys Ile Gly Met Ala Leu Val Ile Ala Pro Trp Ser Met Leu Arg Ala  
           65                  70                  75                  80  
 Ile Lys Leu Val Ser His Leu Pro Pro Gly Tyr Glu Arg Ser Ile Trp  
                   85                  90                  95  
 Glu Ala Thr

<210> 153  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 153  
 ggctggcggtt tcccacattt ctctgtggga gggtccttga gaggacacag ggatgaaptg 60  
 gtgactctgt ccagaccct tggacagaga agcctatgcc ggagccacct ctactacag 120  
 gtctctgagct tgggtgctgag gacgcctgga ggaatcacag agcccatctg gaacagccca 180  
 tctctgggt ggggtggatc agcctctggt ttcttctcag agcactgaga aggtctggct 240  
 caaccaccte caagattcat cttgttctgt ggacacagca tctagtgaca caagacaaga 300  
 gagcaccaaa actctctagg agcacaggaa gtccttcagc tttcaggaat cagaagaggt 360  
 gtcacagctc tgaagaataa ggacttccac aagcccagga gatgagaagg ggtggaagtt 420  
 ggagggggcg gactgggtgg agtggacatt ccaggagctg ggtgaggtaa aaacacggag 480  
 gcaggaaaat gcggagtgtt ttggaaacca taataaaaaa aaaaaaaaaa aaaaaaaaaa 540  
 aaaaaaaaaa a 551

<210> 154  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 154  
 Met Pro Glu Pro Pro Leu Thr Thr Gly Pro Glu Leu Gly Ala Glu Asp  
           1                  5                  10                  15  
 Ala Trp Arg Asn His Arg Ala His Leu Glu Gln Pro Ile Ser Trp Leu  
                   20                  25                  30  
 Gly Trp Ile Ser Leu Trp Phe Leu Leu Arg Ala Leu Arg Arg Ser Gly  
           35                  40                  45

Ser Thr Thr Ser Lys Ile His Leu Val Leu Trp Thr Gln His Leu Val  
50 55 60

Thr Gln Asp Lys Arg Ala Pro Lys Leu Ser Arg Ser Thr Gly Ser Pro  
65 70 75 80

Ser Ala Phe Arg Asn Gln Lys Arg Cys His Ser Ser Glu Glu  
85 90

<210> 155

<211> 888

<212> DNA

<213> Homo sapiens

<400> 155

gcccgcgccc aggaagggga tgcggaaacc cctggctcgg tggagcggag aggcaggcgg 60  
ggtgaggggc gttgccaggc aaagggcgag cgcggtggct ggggagccga ggacggcatg 120  
tcccaggccc cgggagcaca gccgagccca cccaccgtgt accacgaacg gcagcgctg 180  
gagctgtgtg ctgtccacgc cctcaacaac gttctgcagc agcagctctt tagccaggag 240  
gctgccgatg agatctgcaa gaggttgccc ccagactccc ggctgaaccc tcatcgcagc 300  
ctcctgggca ccggcaacta tgatgtcaat gtgatcatgg ccgctctgca ggggctgggc 360  
ctggccgccc tgtggtggga caggaggagg cccctgtccc agctggccct gccccaggtg 420  
ctggggctga tcctgaacct gccctcgccc gtgtcgctgg ggctgctgtc actgccgctg 480  
cgccggcggc actgggtggc cctgcgccag gtggacggtg tctactacaa cctggactcc 540  
aagctgcggg cgcgcaggc cctgggggat gaggacggag tcagggcctt cctggcggt 600  
gcgctggccc agggcctgtg cgaggtgctg ctggtagtga ccaaggaggt ggaggagaag 660  
ggcagctggc tgcggacaga ctgacctgg ctgaccatcg gcgcccacag cgcagtccct 720  
gcgcatcccc ctccggtgcy cacactgcat gcctgggaaa ggccagcact tcatggaccc 780  
tggggaggcc ccgccccctc ccacacccc tgctcccac tgcgctgct gcctcaataa 840  
atctgctgat ttgctgcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 888

<210> 156

<211> 188

<212> PRT

<213> Homo sapiens

<400> 156

Met Ser Gln Ala Pro Gly Ala Gln Pro Ser Pro Pro Thr Val Tyr His  
1 5 10 15

Glu Arg Gln Arg Leu Glu Leu Cys Ala Val His Ala Leu Asn Asn Val  
20 25 30

Leu Gln Gln Gln Leu Phe Ser Gln Glu Ala Ala Asp Glu Ile Cys Lys  
35 40 45

Arg Leu Ala Pro Asp Ser Arg Leu Asn Pro His Arg Ser Leu Leu Gly  
50 55 60

Thr Gly Asn Tyr Asp Val Asn Val Ile Met Ala Ala Leu Gln Gly Leu  
65 70 75 80

Gly Leu Ala Ala Val Trp Trp Asp Arg Arg Arg Pro Leu Ser Gln Leu  
85 90 95

Ala Leu Pro Gln Val Leu Gly Leu Ile Leu Asn Leu Pro Ser Pro Val  
100 105 110

Ser Leu Gly Leu Leu Ser Leu Pro Leu Arg Arg Arg His Trp Val Ala

115                      120                      125  
 Leu Arg Gln Val Asp Gly Val Tyr Tyr Asn Leu Asp Ser Lys Leu Arg  
 130                      135                      140  
 Ala Pro Glu Ala Leu Gly Asp Glu Asp Gly Val Arg Ala Phe Leu Ala  
 145                      150                      155                      160  
 Ala Ala Leu Ala Gln Gly Leu Cys Glu Val Leu Leu Val Val Thr Lys  
 165                      170                      175  
 Glu Val Glu Glu Lys Gly Ser Trp Leu Arg Thr Asp  
 180                      185

&lt;210&gt; 157

&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 157

gaaacactga atatttcaac agcagaaatt gaatgggggg attgatagcg ctggcgaggg 60  
 aagcagctgg aaagagacag atggcaccct gagacagccc agagggtgaat aggaccccca 120  
 ggctgcaggg ataaagctca gtggtgggtg tacctcaccg gggaccaggg tcacacagca 180  
 aagctggaac aacagaggcg tgttggtggg gagcctcaga ggggacaaaa cctctgcctg 240  
 agatcccacc ccaggtgggc atggggggcca ctgaggttgg ggatgaaaat gccggtaccg 300  
 tcagtgcaca gccctgttcc agacagtgcg gcctggaaga tttctgggct ctcctgaggc 360  
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 tcccttctac cctagctgtc ttcttgaact tgggactctc ctttcccaag acttccatca 480  
 ctagctcctg gagggactgg accttgcatc ttcccttcgc gtggagcctc agtgtgagag 540  
 gccctgccaa tgcgtgcatg tcagagggtg tggggaccac atcagaagaa gaggggggtg 600  
 atgaaattaa caaataaaaa gtatggggaa acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 659

&lt;210&gt; 158

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

Met Gly Ala Thr Glu Val Gly Asp Glu Asn Ala Gly Thr Val Ser Ala  
 1                      5                      10                      15  
 Gln Pro Cys Ser Arg Gln Cys Cys Leu Glu Asp Phe Trp Ala Leu Leu  
 20                      25                      30  
 Arg Arg His Pro Ala Pro Glu Pro Pro Trp Thr Pro Val Leu Tyr  
 35                      40                      45  
 Pro Leu Arg Thr Ser Leu Pro Ser Thr Leu Ala Val Phe Leu Asn Leu  
 50                      55                      60  
 Gly Leu Ser Phe Pro Lys Thr Ser Ile Thr Ser Ser Trp Arg Asp Trp  
 65                      70                      75                      80  
 Thr Leu His Leu Pro Phe Ala Trp Ser Leu Ser Val Arg Gly Pro Ala  
 85                      90                      95  
 Asn Ala Cys Met Ser Glu Val Val Gly Thr Thr Ser Glu Glu Gly  
 100                      105                      110

Gly Asp Glu Ile Asn Lys  
115

<210> 159  
<211> 550  
<212> DNA  
<213> Homo sapiens

<400> 159  
ccttgagtct cccggccgcc ttgccatggc tgcccgtggt gtcacgctc cagttggcga 60  
gagtttgccg tacgctgagt acttgcagcc ctccggccaaa cggccagacg ccgacgtcga 120  
ccagcagaga ctggtaagaa gtttgatagc tgtaggcctg ggtgttgacg ctcttgcat 180  
tgcaggtcgc tacgcatttc ggatctggaa acctctagaa caagttatca cagaaactgc 240  
aaagaagatt tcaactccta gcttttcatc ctactataaa ggaggatttg aacagaaaat 300  
gagtaggcga gaagctggtc ttattttagg tgtaagccca tctgctggca aggctaagat 360  
tagaacagct cataggagag tcatgatatt gaatcaccca gataaagggt gatctcctta 420  
cgtagcagcc aaaataaatg aagcaaaaga cttgctagaa acaaccacca aacattgatg 480  
cttaaggacc acactgaagg aaaaaaaaaa aggggactcc aaaaaaaaaa aaaaaaaaaa 540  
aaaaaaaaa 550

<210> 160  
<211> 150  
<212> PRT  
<213> Homo sapiens

<400> 160  
Met Ala Ala Arg Gly Val Ile Ala Pro Val Gly Glu Ser Leu Arg Tyr  
1 5 10 15  
Ala Glu Tyr Leu Gln Pro Ser Ala Lys Arg Pro Asp Ala Asp Val Asp  
20 25 30  
Gln Gln Arg Leu Val Arg Ser Leu Ile Ala Val Gly Leu Gly Val Ala  
35 40 45  
Ala Leu Ala Phe Ala Gly Arg Tyr Ala Phe Arg Ile Trp Lys Pro Leu  
50 55 60  
Glu Gln Val Ile Thr Glu Thr Ala Lys Lys Ile Ser Thr Pro Ser Phe  
65 70 75 80  
Ser Ser Tyr Tyr Lys Gly Gly Phe Glu Gln Lys Met Ser Arg Arg Glu  
85 90 95  
Ala Gly Leu Ile Leu Gly Val Ser Pro Ser Ala Gly Lys Ala Lys Ile  
100 105 110  
Arg Thr Ala His Arg Arg Val Met Ile Leu Asn His Pro Asp Lys Gly  
115 120 125  
Gly Ser Pro Tyr Val Ala Ala Lys Ile Asn Glu Ala Lys Asp Leu Leu  
130 135 140  
Glu Thr Thr Thr Lys His  
145 150

<210> 161  
<211> 622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 161

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ctcacctgtg ctgccacttc ctagtgcaca cctcacggtt catcctcaag ctggaagata 60
cctctctggc cccggcacat gtcacccctg cactcctgcc ttcccgtggg cacttccaca 120
tcctctgggc ctctggcagt tcccaggac tgttttcacc tctgctgtct ctgggggtcag 180
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aaaaaaaaa aaaaaaaaaa aa                                     622

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&lt;210&gt; 162

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 162

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Met Ser Pro Leu His Ser Cys Leu Pro Val Gly Thr Ser Thr Ser Ser
  1              5              10              15

Gly Pro Leu Ala Val Pro Arg Asp Cys Phe His Leu Cys Cys Leu Trp
      20              25              30

Gly Gln Leu Leu Leu Ile Ser Cys Pro Leu Ala Cys Gly Gln Gly Cys
  35              40              45

Arg Val Ala Gly Gly Gln Gln His Val Pro Gly Gln Ala Leu Gly Thr
  50              55              60

Leu Ser Pro Leu Val Ser Leu Leu Thr Trp Ala Gly Pro Ser Leu Asp
  65              70              75              80

Trp Pro His Pro Gly Ser Leu Val Thr Pro Arg Cys Pro Ile Leu Pro
      85              90              95

Ala Val Pro Val Leu Val Lys Gly Leu Gly Gly Trp Pro Pro Thr Arg
      100              105              110

Pro Ser Arg Ala Ala Pro Val Ser Gly Pro Trp Asp Gln Leu Pro Tyr
      115              120              125

Phe Pro Gly Leu
      130

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&lt;210&gt; 163

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 163

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ctcgtttctc tgcattacac gccggtcagg attcgcgacc cgacatggag cgtccccgca 60
gtccccaatg ctcgcccccg gcctctgcct cagcttcggt taccctggcg cagctcctgc 120
agctgggtcca gcagggccag gaactcccgg gcctggagaa acgccacatc gcggcgatcc 180
acggcgaacc cacagcgtcc cggctgccgc ggaggcccaa gccctgggag gccgcggctt 240

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tggttgagtc ccttccccct cgcacctca ggataggaac ggccccggcg gagcctggct 300  
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 ccttttgcggc ggcgatctgg agggcggtggc tacaggaccc gggatgccat tcagttactc 420  
 atcttttatg ctttcgtcct gacctgtctc aactagactt gctcctgcaa ccaccatggg 480  
 ggtttttgcac ttacatttgt ggaccatgtt acagttaaga aaaatcctgt ttcagtcctt 540  
 atatgtaata aaatgtttta tgatggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 596

<210> 164

<211> 101

<212> PRT

<213> Homo sapiens

<400> 164

Met Glu Arg Pro Arg Ser Pro Gln Cys Ser Ala Pro Ala Ser Ala Ser  
 1 5 10 15

Ala Ser Val Thr Leu Ala Gln Leu Leu Gln Leu Val Gln Gln Gly Gln  
 20 25 30

Glu Leu Pro Gly Leu Glu Lys Arg His Ile Ala Ala Ile His Gly Glu  
 35 40 45

Pro Thr Ala Ser Arg Leu Pro Arg Arg Pro Lys Pro Trp Glu Ala Ala  
 50 55 60

Ala Leu Ala Glu Ser Leu Pro Pro Pro Thr Leu Arg Ile Gly Thr Ala  
 65 70 75 80

Pro Ala Glu Pro Gly Leu Val Glu Ala Ala Thr Ala Pro Ser Ser Trp  
 85 90 95

His Thr Val Gly Pro  
 100

<210> 165

<211> 670

<212> DNA

<213> Homo sapiens

<400> 165

cttagaaagc ggcggtgagg tcagcttcac attctcagga actctccttc tttgggtctg 60  
 gctgaagttg aggatctctt actctctagg ccacggaatt aacccgagca ggcattggagg 120  
 cctctgctct cacctcatca gcagtgacca gtgtggccaa agtggtcagg gtggcctctg 180  
 gctctgccgt agttttgccc ctggccagga ttgtacagt tgtgattgga ggagttgttg 240  
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 tagcagccaa gatgatgtcc ggcgcggcca ttgccaatgg ggtgggagtt gcctcgggca 360  
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 tcctgggctc cattgggtct gccattgcgg ctgtcattgc gaggttctac tagctcctg 480  
 cccctcgccc tgcagagaag agaaccatgc caggggagaa ggcacccagc catcctgacc 540  
 cagcgaggag ccaactatcc caaatatacc tggggtgaaa tataccaaat tctgcatctc 600  
 cagaggaaaa taagaaataa agatgaattg ttgcaactat aaaaaaaaaa aaaaaaaaaa 660  
 aaaaaaaaaa 670

<210> 166

<211> 119

<212> PRT

<213> Homo sapiens

<400> 166

Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys  
 1 5 10 15

Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg  
 20 25 30

Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu  
 35 40 45

Ser Ala Met Gly Phe Thr Ala Gly Gly Ile Ala Ser Ser Ser Ile Ala  
 50 55 60

Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala  
 65 70 75 80

Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu  
 85 90 95

Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala  
 100 105 110

Ala Val Ile Ala Arg Phe Tyr  
 115

<210> 167  
 <211> 850  
 <212> DNA  
 <213> Homo sapiens

<400> 167  
 caaacttaca cagtgccttg ggaattccaa agtactcagt ggagagaggt gtttcaggag 60  
 ccgtagagcc agatcgatcat catgtctgca ttgtggctgc tgctgggcct ccttgccctg 120  
 atggacttgt ctgaaagcag caactgggga tgctatggaa acatccaaag cctggacacc 180  
 cctggagcat cttgtgggat tggaagacgt cacggcctga actactgtgg agttcgtgct 240  
 tctgaaaggc tggctgaaat agacatgcca tacctcctga aatatcaacc catgatgcaa 300  
 accattggcc aaaagtactg catggatcct gccgtgatcg ctggtgtctt gtccaggaag 360  
 tctcccggtg acaaaattct ggtcaacatg ggcatagga ctagcatggt gcaggaccct 420  
 ggctctcaag ctcccacatc ctggattagt gagtctcagg tttcccagac aactgaagtt 480  
 ctgactacta gaatcaaaga aatccagagg aggtttccaa cctggacccc tgaccagtac 540  
 ctgagagggt gactctgtgc ctacagtggg ggtgctggct atgtccgaag cagccaggac 600  
 ctgagctgtg acttctgcaa tgatgtcctt gcacgagcca agtacctcaa gagacatggc 660  
 ttctaacatc tcagatgaaa cccaagacca tgatcacata tgcagcctca aatgttacac 720  
 agataaaact agccaagggc acctgtaact gggaatctga gtttgaccta aaagtcatta 780  
 aaataacatg aatcacatta aaggaagaat tttgacctgc aaaaaaaaaa aaaaaaaaaa 840  
 aaaaaaaaaa 850

<210> 168  
 <211> 194  
 <212> PRT  
 <213> Homo sapiens

<400> 168  
 Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu  
 1 5 10 15

Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp  
 20 25 30

Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr

35                      40                      45  
 Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr  
     50                      55                      60  
 Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys  
     65                      70                      75                      80  
 Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly  
                     85                      90                      95  
 Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp  
                     100                      105                      110  
 Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser  
                     115                      120                      125  
 Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg  
     130                      135                      140  
 Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala  
     145                      150                      155                      160  
 Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys  
                     165                      170                      175  
 Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His  
                     180                      185                      190

Gly Phe

<210> 169

<211> 494

<212> DNA

<213> Homo sapiens

<400> 169

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 atgccatttt tgcaggattt cttcgtgatt tctgtccata tgaaaatgct gacattaaac 180  
 attaacacat ggagaccgtg ccctgtggcc ctgccgtggc tgccagcatg gtctgtgttt 240  
 ccttgtggat tcacctgtgg ccctgctgtg gccaccagca tggctctgtg cctcgtggat 300  
 tcaactgcagc tgtcggatgc gagtttctgt cataatcatt tgtttcctga tacaattgtt 360  
 cttattcttt tccaaaactg taaaataatc tcctccctca aatgcaaagg ttgtttttgt 420  
 tctgtttctg ttttctttga aataaaatta taacgttaaa agacaaaaaa aaaaaaaaaa 480  
 aaaaaaaaaa aaaa 494

<210> 170

<211> 110

<212> PRT

<213> Homo sapiens

<400> 170

Met Pro Phe Leu Gln Asp Phe Phe Val Ile Ser Val His Met Lys Met  
     1                      5                      10                      15  
 Leu Thr Leu Asn Ile Asn Thr Trp Arg Pro Cys Pro Val Ala Leu Pro  
                     20                      25                      30

Trp Leu Pro Ala Trp Ser Val Phe Pro Cys Gly Phe Thr Cys Gly Pro  
           35                          40                          45  
 Ala Val Ala Thr Ser Met Val Cys Val Leu Val Asp Ser Leu Gln Leu  
           50                          55                          60  
 Ser Asp Ala Ser Phe Cys His Asn His Leu Phe Pro Asp Thr Ile Val  
           65                          70                          75                          80  
 Leu Ile Leu Phe Gln Asn Cys Lys Ile Ile Ser Ser Leu Lys Cys Lys  
                           85                          90                          95  
 Gly Cys Phe Cys Ser Val Ser Val Phe Phe Glu Ile Lys Leu  
                           100                          105                          110

&lt;210&gt; 171

&lt;211&gt; 2262

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

gtgctcagtg ttcacgctat atcccttggg caatgtgggg ttggatgggg ccccccacttc 60  
 cattcccatg gaaggaggcc aggtcccccag ccacctccca ctcagccatg cagcacttg 120  
 ctgggctggc ctccctgggaa acacaggtga ctggaatgaa ctctgcattt tcaacgtgcc 180  
 ttctactgct tcaggacctg ggggtccccc tgacctcac tggtttgccc ccagccctgg 240  
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 ccgctgacgg ccaatggggc ttggggccag gggcagagaa ccccaacagc aagagagccc 1140  
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 aatggtgttg attgcagact ggaggggtaa cctccgctga gggtcattat gtgccaggca 1920  
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 agtgatgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2160  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2220

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa

2262

&lt;210&gt; 172

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

Met Trp Gly Trp Met Gly Pro Pro Leu Pro Phe Pro Trp Lys Glu Ala  
 1 5 10 15

Arg Ser Pro Ala Thr Ser His Ser Ala Met His Ala Leu Ala Gly Leu  
 20 25 30

Ala Ser Trp Glu Thr Gln Val Thr Arg Met Asn Ser Ala Phe Ser Thr  
 35 40 45

Cys Leu Leu Leu Leu Gln Asp Leu Gly Val Pro Leu Thr Leu Thr Gly  
 50 55 60

Leu Pro Pro Ala Leu Gly Leu Ala Pro Pro Val Leu Glu Pro Arg Ala  
 65 70 75 80

Pro Gly Leu Glu Leu Pro Leu Trp Gly Gly Ser Gln Ala Pro Pro Leu  
 85 90 95

Pro Leu Leu Ser Ser Val Pro Cys Ser Ala Pro Pro Met Tyr Leu Ser  
 100 105 110

Val Phe Arg Pro Leu Thr Glu Arg Arg Cys Arg Val Ser Arg Gly Pro  
 115 120 125

Arg Trp Ser Gln Gly Gln Gly Trp Asp Leu Gln Gly Thr Arg Gly Ala  
 130 135 140

His Gly Leu Arg His Leu Cys Pro Gly Ser  
 145 150

&lt;210&gt; 173

&lt;211&gt; 2538

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

gaaaagtgga gatagttcct gtctcatgga ttgctagggg gattaagagg agtgcctgta 60  
 gaacacatag ctacagtgct agtgcacagc aggtgtgtcc cagaggtgag ctgtggttgt 120  
 tagtctttgt gaggtagag ctgggctagg tccaggcct gactctgtct gatgttgttt 180  
 ctctctgca ctgtagtact ttattcccag attctgcttt ttaattcttt ttggtgtaa 240  
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 ggtctggctg tggggcatag tgggttcccc tagggctggg ggagggtggg gagggaggag 360  
 ggtgtgggct gcctcgggtgc atctctctga caggctctgg ccctgggtca gtccaagatg 420  
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 cacccccacc tcttccttag ttattgggct gggagtgtct gtcagactcc aatatccaga 540  
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 ggagttctag agctggtagg tgtagctgc cgacctacc gcccttcta cacaccttgc 840  
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2538

```

&lt;210&gt; 174

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 174

```

Met Thr Pro Val Trp Pro Ile Val Arg Gly Arg Trp Asp Glu Val Cys
 1             5             10            15

Arg Ile Ser Leu Lys Thr Gly Met Ala Val Pro Val Phe Gly Trp Trp
 20             25            30

Leu Val Gly Leu Ser Ile Phe Ile Gly Cys Pro Leu Cys Ser Gln Cys
 35             40            45

Trp Val Leu Pro Trp Asp Thr Met Glu Asn Gln Gln Met Glu Pro Leu
 50             55            60

Pro Pro Arg Ser Ser Gln Pro Gly Gly Ser Val Phe Ala Gly Ser Pro
 65             70            75            80

Phe Arg Leu Ala Gly Phe Pro Gly Leu Cys Ala Ala Ser Ala Pro Tyr
 85             90            95

His Leu Leu Ser Val Leu Gly Arg Leu Gln Phe Ser Ser Gln Ser Gln
100            105            110

Pro His Asp Leu Arg Gln Ser His Pro Ala Leu Val Cys
115            120            125

```

<210> 175  
 <211> 2371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (285)

<400> 175  
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 ctatcttagc tgtctttccc agcgggtgcta agagtgggtc cagtgagaag gtagatgccca 360  
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 cagagctgct agagaccatc ctgcccatcc gagttctgag attgggactg tgatgttggg 480  
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 tgcttccaca cccctggccg tgagaacgtg gtatgtagga gaggttggtg tagctttagg 600  
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 tgtcctccaa atgctgctgt tgggagcggg ctccagctc tcagtggcag tgcacctctc 1140  
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<210> 176  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 176  
 Met Cys Gly Ile Ile Ser Leu Gln Pro Pro Asn Ser Ile Ser Pro Leu  
 1 5 10 15

Gln Pro Asp Ser Leu Ala Asp Ala His Cys Ser Leu Ser Ile Pro Thr  
 20 25 30

Lys Phe Ser Phe Ile Ser Ser Leu Lys Val Leu Ile Ser Asn Lys Tyr  
 35 40 45

Ile Arg Lys Ile Met Phe Leu Leu Ser His Leu Thr Phe Ser Ser Gln  
 50 55 60

Ile Ser Pro Phe Leu Glu His Ser Leu Cys Leu Ala Leu Met Phe Thr  
 65 70 75 80

Ser Tyr Phe Leu Glu Val Gln Lys Ser Gln Phe Val Ser Val Tyr Ser  
 85 90 95

Ser Leu Ser Ser Leu Leu Thr Ala Arg Gly Ser Val Ser Val Asp Phe  
 100 105 110

Ile Leu

<210> 177  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (1633)

<400> 177  
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 gtccctcgcc ggctccctcg gggcctccac tgcagcgcag ctgcccatac ctctgaacag 240  
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 gaggacctgt ttgggcaggc gcctgggtgg gaacgggaca aggcgagctt cctgcagacg 360  
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 tgttggttgt gcncgaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1665



<210> 178  
 <211> 431  
 <212> PRT  
 <213> Homo sapiens

<400> 178

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Met Ser Trp Val Gln Ala Thr Leu Leu Ala Arg Gly Leu Cys Arg Ala
  1              5              10              15

Trp Gly Gly Thr Cys Gly Ala Ala Leu Thr Gly Thr Ser Ile Ser Gln
      20              25              30

Val Pro Arg Arg Leu Pro Arg Gly Leu His Cys Ser Ala Ala Ala His
      35              40              45

Ser Ser Glu Gln Ser Leu Val Pro Ser Pro Pro Glu Pro Arg Gln Arg
      50              55              60

Pro Thr Lys Ala Leu Val Pro Phe Glu Asp Leu Phe Gly Gln Ala Pro
      65              70              75              80

Gly Gly Glu Arg Asp Lys Ala Ser Phe Leu Gln Thr Val Gln Lys Phe
      85              90              95

Ala Glu His Ser Val Arg Lys Arg Gly His Ile Asp Phe Ile Tyr Leu
      100             105             110

Ala Leu Arg Lys Met Arg Glu Tyr Gly Val Glu Arg Asp Leu Ala Val
      115             120             125

Tyr Asn Gln Leu Leu Asn Ile Phe Pro Lys Glu Val Phe Arg Pro Arg
      130             135             140

Asn Ile Ile Gln Arg Ile Phe Val His Tyr Pro Arg Gln Gln Glu Cys
      145             150             155             160

Gly Ile Ala Val Leu Glu Gln Met Glu Asn His Gly Val Met Pro Asn
      165             170             175

Lys Glu Thr Glu Phe Leu Leu Ile Gln Ile Phe Gly Arg Lys Ser Tyr
      180             185             190

Pro Met Leu Lys Leu Val Arg Leu Lys Leu Trp Phe Pro Arg Phe Met
      195             200             205

Asn Val Asn Pro Phe Pro Val Pro Arg Asp Leu Pro Gln Asp Pro Val
      210             215             220

Glu Leu Ala Met Phe Gly Leu Arg His Met Glu Pro Asp Leu Ser Ala
      225             230             235             240

Arg Val Thr Ile Tyr Gln Val Pro Leu Pro Lys Asp Ser Thr Gly Ala
      245             250             255

Ala Asp Pro Pro Gln Pro His Ile Val Gly Ile Gln Ser Pro Asp Gln
      260             265             270

Gln Ala Ala Leu Ala Arg His Asn Pro Ala Arg Pro Val Phe Val Glu
      275             280             285

```

Gly Pro Phe Ser Leu Trp Leu Arg Asn Lys Cys Val Tyr Tyr His Ile  
 290 295 300  
 Leu Arg Ala Asp Leu Leu Pro Pro Glu Glu Arg Glu Val Glu Glu Thr  
 305 310 315 320  
 Pro Glu Glu Trp Asn Leu Tyr Tyr Pro Met Gln Leu Asp Leu Glu Tyr  
 325 330 335  
 Val Arg Ser Gly Trp Asp Asn Tyr Glu Phe Asp Ile Asn Glu Val Glu  
 340 345 350  
 Glu Gly Pro Val Phe Ala Met Cys Met Ala Gly Ala His Asp Gln Ala  
 355 360 365  
 Thr Met Ala Lys Trp Ile Gln Gly Leu Gln Glu Thr Asn Pro Thr Leu  
 370 375 380  
 Ala Gln Ile Pro Val Val Phe Arg Leu Ala Gly Ser Thr Arg Glu Leu  
 385 390 395 400  
 Gln Thr Ser Ser Ala Gly Leu Glu Glu Pro Pro Leu Pro Glu Asp His  
 405 410 415  
 Gln Glu Glu Asp Asp Asn Leu Gln Arg Gln Gln Gln Gly Gln Ser  
 420 425 430

&lt;210&gt; 179

&lt;211&gt; 2080

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 179

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<210> 180

<211> 342

<212> PRT

<213> Homo sapiens

<400> 180

Met Arg Lys Glu Thr Pro Pro Pro Leu Val Pro Pro Ala Ala Arg Glu  
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 Trp Asn Leu Pro Pro Asn Ala Pro Ala Cys Met Glu Arg Gln Leu Glu  
 20 25 30  
 Ala Ala Arg Tyr Arg Ser Asp Gly Ala Leu Leu Leu Gly Ala Ser Ser  
 35 40 45  
 Leu Ser Gly Arg Cys Trp Ala Gly Ser Leu Trp Leu Phe Lys Asp Pro  
 50 55 60  
 Cys Ala Ala Pro Asn Glu Gly Phe Cys Ser Ala Gly Val Gln Thr Glu  
 65 70 75 80  
 Ala Gly Val Ala Asp Leu Thr Trp Val Gly Glu Arg Gly Ile Leu Val  
 85 90 95  
 Ala Ser Asp Ser Gly Ala Val Glu Leu Trp Glu Leu Asp Glu Asn Glu  
 100 105 110  
 Thr Leu Ile Val Ser Lys Phe Cys Lys Tyr Glu His Asp Asp Ile Val  
 115 120 125  
 Ser Thr Val Ser Val Leu Ser Ser Gly Thr Gln Ala Val Ser Gly Ser  
 130 135 140  
 Lys Asp Ile Cys Ile Lys Val Trp Asp Leu Ala Gln Gln Val Val Leu  
 145 150 155 160  
 Ser Ser Tyr Arg Ala His Ala Ala Gln Val Thr Cys Val Ala Ala Ser  
 165 170 175  
 Pro His Lys Asp Ser Val Phe Leu Ser Cys Ser Glu Asp Asn Arg Ile  
 180 185 190  
 Leu Leu Trp Asp Thr Arg Cys Pro Lys Pro Ala Ser Gln Ile Gly Cys  
 195 200 205  
 Ser Ala Pro Gly Tyr Leu Pro Thr Ser Leu Ala Trp His Pro Gln Gln  
 210 215 220  
 Ser Glu Val Phe Val Phe Gly Asp Glu Asn Gly Thr Val Ser Leu Val

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<210> 182
<211> 91
<212> PRT
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&lt;213&gt; Homo sapiens

&lt;400&gt; 182

```

Met Lys Pro Ser Ala Val Gln Pro Leu Pro Phe Phe Leu Leu Ser Phe
 1             5             10             15

Phe Leu Leu Arg Ala Val Gly Gly Val Ser Thr Ala Ala Gly Gly Gly
          20             25             30

Gly Gly Gly Glu Lys Glu Ser Gly Tyr Arg Ser Ala Ser Phe Leu Ala
          35             40             45

Leu Ala Gly Pro Ala Arg Glu Leu Leu Val Phe Val Thr Val Leu Ala
          50             55             60

Ala Leu Phe Cys Gln Pro Ser Leu Ser Ala Tyr Trp Leu Gly Ala Lys
          65             70             75             80

Ala Gly Gly Gly Leu Leu Ile Leu Ser Val Ala
          85             90

```

&lt;210&gt; 183

&lt;211&gt; 1484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 183

```

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```

&lt;210&gt; 184

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

Met Ser Asp Ile Val Asn Phe Tyr Leu Val Gly Cys Cys Ile Phe Leu  
 1 5 10 15

Tyr Ser Cys Lys Cys Tyr Thr Leu Phe Cys His Thr Ile Lys Leu Val  
 20 25 30

Gly Asn Asn Phe Ile Phe Leu Arg Tyr Gly Arg Trp Val Trp Ser Ser  
 35 40 45

Ala Gln Pro Arg Thr Asp Leu Leu Thr Ser Lys Ala Arg Pro Phe  
 50 55 60

Tyr Ala Val Tyr Pro Leu Leu Tyr Val Ser Cys Ser Phe Phe Ser Leu  
 65 70 75 80

Ala Glu Gly Thr Gly Val Gly Ala Gly Pro Phe Val His Gln Ala Phe  
 85 90 95

Val Ile Thr Glu Leu Ser Phe Gly Ser Phe Pro Gly Phe Leu Ser Phe  
 100 105 110

Leu His Thr Cys Gly Leu Ile Ser Ile His Gln Asn Thr  
 115 120 125

&lt;210&gt; 185

&lt;211&gt; 2520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

cccgagtgc tctggaatac gcagagtcag taagaccatg gctacgtcct cgatgtctaa 60  
 ggggttgcttt gtttttaagc caaactccaa aaagagaaaag atctctctgc caatagagga 120  
 ctattttaac aaagggaaaa atgagcctga ggacagtaag ctctcgattcg aaacttatca 180  
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 tgtcacacca tatgtagtct cattgcaagc taaagattgt ccagatatga aacatttttt 480  
 gcaaaagtgt atctcacagt tgatggactg ctgtgtagat ataaaatcca aagaggagga 540  
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 agtactacaa gacttcataa ttatcagcag tcaacatctc catgaatttc cactaatact 780  
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 tctaccatct tttaggaggt acgtggaaaa gcaagcttca gaaaagcaag ttgcgctctt 1200  
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 aaaacacctg tggagtactt tagactccaa caaataataa tgtaactaaa actgctcaca 2400  
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<210> 186

<211> 711

<212> PRT

<213> Homo sapiens

<400> 186

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 Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg Phe Glu Thr Tyr Gln  
 35 40 45  
 Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu Arg Leu Gln Glu Glu  
 50 55 60  
 Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu Phe Leu Gln Lys Ser  
 65 70 75 80  
 His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu Gly Gly Gln Ile Lys  
 85 90 95  
 Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu Gly Val Asn Val Thr  
 100 105 110  
 Asp His Asp Leu Thr Phe Gly Ser Leu Thr Glu Ala Leu Gln Asn Asn  
 115 120 125  
 Val Thr Pro Tyr Val Val Ser Leu Gln Ala Lys Asp Cys Pro Asp Met  
 130 135 140  
 Lys His Phe Leu Gln Lys Leu Ile Ser Gln Leu Met Asp Cys Cys Val  
 145 150 155 160  
 Asp Ile Lys Ser Lys Glu Glu Glu Ser Val His Val Thr Gln Arg Lys  
 165 170 175  
 Thr His Tyr Ser Met Asp Ser Leu Ser Ser Trp Tyr Met Thr Val Thr  
 180 185 190  
 Gln Lys Thr Asp Pro Lys Met Leu Ser Lys Lys Arg Thr Thr Ser Ser  
 195 200 205  
 Gln Trp Gln Ser Pro Pro Val Val Ile Leu Lys Asp Met Glu Ser

210	215	220
Phe Ala Thr Lys Val Leu Gln Asp Phe Ile Ile Ile Ser Ser Gln His		
225	230	235 240
Leu His Glu Phe Pro Leu Ile Leu Ile Phe Gly Ile Ala Thr Ser Pro		
	245	250 255
Ile Ile Ile His Arg Leu Leu Pro His Ala Val Ser Ser Leu Leu Cys		
	260	265 270
Ile Glu Leu Phe Gln Ser Leu Ser Cys Lys Glu His Leu Thr Thr Val		
	275	280 285
Leu Asp Lys Leu Leu Leu Thr Thr Gln Phe Pro Phe Lys Ile Asn Glu		
	290	295 300
Lys Val Leu Gln Val Leu Thr Asn Ile Phe Leu Tyr His Asp Phe Ser		
	305	310 315 320
Val Gln Asn Phe Ile Lys Gly Leu Gln Leu Ser Leu Leu Glu His Phe		
	325	330 335
Tyr Ser Gln Pro Leu Ser Val Leu Cys Cys Asn Leu Pro Glu Ala Lys		
	340	345 350
Arg Arg Ile Asn Phe Leu Ser Asn Asn Gln Cys Glu Asn Ile Arg Arg		
	355	360 365
Leu Pro Ser Phe Arg Arg Tyr Val Glu Lys Gln Ala Ser Glu Lys Gln		
	370	375 380
Val Ala Leu Leu Thr Asn Glu Arg Tyr Leu Lys Glu Glu Thr Gln Leu		
	385	390 395 400
Leu Leu Glu Asn Leu His Val Tyr His Met Asn Tyr Phe Leu Val Leu		
	405	410 415
Arg Cys Leu His Lys Phe Thr Ser Ser Leu Pro Lys Tyr Pro Leu Gly		
	420	425 430
Arg Gln Ile Arg Glu Leu Tyr Cys Thr Cys Leu Glu Lys Asn Ile Trp		
	435	440 445
Asp Ser Glu Glu Tyr Ala Ser Val Leu Gln Leu Leu Arg Met Leu Ala		
	450	455 460
Lys Asp Glu Leu Met Thr Ile Leu Glu Lys Cys Phe Lys Val Phe Lys		
	465	470 475 480
Ser Tyr Cys Glu Asn His Leu Gly Ser Thr Ala Lys Arg Ile Glu Glu		
	485	490 495
Phe Leu Ala Gln Phe Gln Ser Leu Asp Glu Thr Lys Glu Glu Glu Asp		
	500	505 510
Ala Ser Gly Ser Gln Pro Lys Gly Leu Gln Lys Thr Asp Leu Tyr His		
	515	520 525
Leu Gln Lys Ser Leu Leu Glu Met Lys Glu Leu Arg Arg Ser Lys Lys		



530                      535                      540  
 Gln Thr Lys Phe Glu Val Leu Arg Glu Asn Val Val Asn Phe Ile Asp  
 545                      550                      555                      560  
 Cys Leu Val Arg Glu Tyr Leu Leu Pro Pro Glu Thr Gln Pro Leu His  
                          565                      570                      575  
 Glu Val Val Tyr Phe Ser Ala Ala His Ala Leu Arg Glu His Leu Asn  
                          580                      585                      590  
 Ala Ala Pro Arg Ile Ala Leu His Thr Ala Leu Asn Asn Pro Tyr Tyr  
                          595                      600                      605  
 Tyr Leu Lys Asn Glu Ala Leu Lys Ser Glu Glu Gly Cys Ile Pro Asn  
                          610                      615                      620  
 Ile Ala Pro Asp Ile Cys Ile Ala Tyr Lys Leu His Leu Glu Cys Ser  
 625                      630                      635                      640  
 Arg Leu Ile Asn Leu Val Asp Trp Ser Glu Ala Phe Ala Thr Val Val  
                          645                      650                      655  
 Thr Ala Ala Glu Lys Met Asp Ala Asn Ser Ala Thr Ser Glu Glu Met  
                          660                      665                      670  
 Asn Glu Ile Ile His Ala Arg Phe Ile Arg Ala Val Ser Glu Leu Glu  
                          675                      680                      685  
 Leu Leu Gly Phe Ile Lys Pro Thr Lys Gln Lys Thr Asp His Val Ala  
                          690                      695                      700  
 Arg Leu Thr Trp Gly Gly Cys  
 705                      710

&lt;210&gt; 187

&lt;211&gt; 3116

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

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 gttagcagca ttgggtgtat gttctcccga actttggatg acacttttca agtggcttcg 120  
 attaagaact gtacacccaa tattgttggtc tcttattctg agcatggccg tgctactat 180  
 aatagggtctc agcttatgga aagagttttt tcccagatta atgacagaat taatggaact 240  
 acaggaattc tatgaccag atacagtgga acttatgacc tggataaaaa ggcaagctcc 300  
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 atggatgggtg acaagtttgc ctctttacaa tgatgatgat cttctcaaga gaaatgaaaa 420  
 tatctaccaa atctattcaa agcgatctgc tgaggatatt tataaaatac tgacatctta 480  
 caaagctaatac taactaattg tagaggatgc tatctgcaat gaggtgggac ccatgagagg 540  
 ctgtaggggt aaagatttat tagacattgc aaatggccac atgggtttgtg aagaagggtga 600  
 caagctaacc tactcaaaat atgggctgatt ttgtcatgag gtcaaaatta actattctcc 660  
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cagatacatt tctcaaacat aacatttaat aaataatgtg atataattat ttaatagaaa 1140  
 gaataattcc gaccttcaag caagtttctg aagggtatatt atgatgtata acaactgaag 1200  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3116

&lt;210&gt; 188

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

Met Val Ile Glu Gly Leu Lys Tyr Ile Trp Ile Pro Tyr Val Cys Met  
 1 5 10 15

Leu Ala Ala Phe Gly Val Cys Ser Pro Glu Leu Trp Met Thr Leu Phe  
 20 25 30

Lys Trp Leu Arg Leu Arg Thr Val His Pro Ile Leu Leu Ala Leu Ile  
 35 40 45

Leu Ser Met Ala Val Pro Thr Ile Ile Gly Leu Ser Leu Trp Lys Glu  
 50 55 60

Phe Phe Pro Arg Leu Met Thr Glu Leu Met Glu Leu Gln Glu Phe Tyr  
 65 70 75 80

Asp Pro Asp Thr Val Glu Leu Met Thr Trp Ile Lys Arg Gln Ala Pro  
 85 90 95

Val Ala Ala Val Phe Ala Gly Ser Pro Gln Leu Met Gly Ala Ile Lys

100                      105                      110  
 Leu Cys Thr Gly Trp Met Val Thr Ser Leu Pro Leu Tyr Asn Asp Asp  
           115                      120                      125  
 Asp Leu Leu Lys Arg Asn Glu Asn Ile Tyr Gln Ile Tyr Ser Lys Arg  
           130                      135                      140  
 Ser Ala Glu Asp Ile Tyr Lys Ile Leu Thr Ser Tyr Lys Ala Asn Tyr  
           145                      150                      155                      160  
 Leu Ile Val Glu Asp Ala Ile Cys Asn Glu Val Gly Pro Met Arg Gly  
                                 165                      170                      175  
 Cys Arg Val Lys Asp Leu Leu Asp Ile Ala Asn Gly His Met Val Cys  
                                 180                      185                      190  
 Glu Glu Gly Asp Lys Leu Thr Tyr Ser Lys Tyr Gly Arg Phe Cys His  
                                 195                      200                      205  
 Glu Val Lys Ile Asn Tyr Ser Pro Tyr Val Asn Tyr Phe Thr Arg Val  
                                 210                      215                      220  
 Tyr Trp Asn Arg Ser Tyr Phe Val Tyr Lys Ile Asn Thr Val Ile Ser  
                                 225                      230                      235                      240

Phe Gln Ser

<210> 189

<211> 839

<212> DNA

<213> Homo sapiens

<400> 189

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 tccaagggag gttgtgtgta tggttcttaa ttcacagga caaagacccc cagcatgtgt 180  
 gtaccctggg acccgatttc tctgggceca catctatctc caatacctca gcctcagatc 240  
 agaccctttc ttttttgtct ttcttctctt aatttttaaa tgcctctttt cttgagcatt 300  
 ccattctctt ttttgacct ctcaggactg ggcttagctg tccagagccc tgccggaggg 360  
 tgctgggggc tgcctctctg caggcactgt gttttctctc ggggctgtcc tcagaacacc 420  
 cctcctgtct cctggggctc ctcaggagc catttcagct ggagtctcag gtctcaaaaa 480  
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 tgcccgcccc tggcagcaag gggcttttgc gcagttggag atgctgccgt tgtggcagag 720  
 cgtcctgcag ccccgcttcc atcagcagc tctgggggtg gggcttttgc ggggatgctc 780  
 tctgatgttt gtccgttgt ttaaataaaa tgcacttatt tttgtttttt tttttgcta 839

<210> 190

<211> 112

<212> PRT

<213> Homo sapiens

<400> 190

Met Pro Leu Phe Leu Ser Ile Pro Ser Leu Phe Leu Thr Leu Ser Gly  
           1                      5                      10                      15

Leu Gly Leu Ala Val Gln Ser Pro Ala Gly Gly Cys Trp Gly Leu Ser  
                   20                  25                  30  
 Leu Cys Arg His Cys Val Phe Leu Arg Gly Cys Pro Gln Asn Thr Pro  
                   35                  40                  45  
 Pro Ala Pro Trp Gly Ser Ser Gly Ser His Phe Ser Trp Ser Leu Arg  
                   50                  55                  60  
 Ser Gln Lys Gln Leu Leu Gln Glu Ala Lys Lys Arg Leu Gly Trp Leu  
                   65                  70                  75                  80  
 Leu Val Leu Met Thr Ala Phe Ile Leu Leu Gly His Phe Gly Tyr Ile  
                   85                  90                  95  
 His Gly His Cys Phe His Leu Ser Phe Leu Pro Val Pro Pro Leu Pro  
                   100                  105                  110

<210> 191  
 <211> 491  
 <212> DNA  
 <213> Homo sapiens

<400> 191  
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 atttttttga ggagaagcag cccctgcagt tccacgtgtt cgatgccgag gacggagcca 180  
 ccagccctag cccgtgactg cctccctccg gaccgacact cctcagcct ctcagtgcct 240  
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 tgctgtggcc ctcagtgac ttccttgggt gatcctgact ttctagccat taataaagag 420  
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 aaaaaaaaaa a 491

<210> 192  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 192  
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 Asp Arg His Ser Leu Ser Leu Ser Val Pro Val Leu Thr Leu Val Thr  
                   20                  25                  30  
 Pro Val Thr Asn Ala Ser Thr Ser Trp Thr Arg Cys Ala Pro Trp Val  
                   35                  40                  45  
 Leu Asp Val Ser Gly Gly Ser Cys Ser Tyr Leu Ser Lys Pro His Thr  
                   50                  55                  60  
 Leu Gln Cys Cys Gly Pro Ser Val Thr Ser Leu Gly Asp Pro Asp Phe  
                   65                  70                  75                  80  
 Leu Ala Ile Asn Lys Glu Asn Cys Ser  
                   85

<210> 193  
 <211> 2619  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
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 atttaacgga tatcgtacta ttctctcatc ccacaggggtc aggctgtgcc acatccaccc 180  
 agccttgccct ggggtcattt atcctacatg tactcagatc acgtgaactg gtgatggggcc 240  
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 tgcttgaagg taagctttat atagattttt agagatactt ggtaaatgag aaaatggaaa 1980  
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 <212> PRT  
 <213> Homo sapiens

<400> 194  
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 Ile Ser Arg Val Pro Glu Gln Thr Thr Met Ala Phe Gln Asp Gly Asn  
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 Pro Arg Glu Gln Leu Ser Arg Pro Gln Lys Ala Ser Leu Ser Val Gln  
                   50                  55                  60  
 Gly Arg Ser Gly Pro Met His Gln Val Gly His Glu Leu Gln Cys Leu  
                   65                  70                  75                  80  
 Leu Trp Gly Met Thr His Ile Tyr Arg Val Trp Ala Ser Glu Pro Ser  
                   85                  90                  95  
 Ala Pro Lys Thr Asp Leu Ser Gln Leu Ser Leu Trp Phe Ser Gln Ala  
                   100                  105                  110  
 Ser Arg Thr Trp Gly Leu Met Gly Ala Glu Gly Phe Pro Ser Gly Ser  
                   115                  120                  125  
 Ala Ser Ile Cys Arg Thr Val Gly Thr Ser Ala Ser Ile Arg Pro Leu  
                   130                  135                  140  
 Pro Ile Phe Trp Ser Ala Arg Gly Leu Leu Leu Phe Pro Pro Phe Pro  
                   145                  150                  155                  160  
 Leu Val Met Asp Ile Tyr Leu Thr Phe Thr Pro Pro Pro Phe Ser Phe  
                   165                  170                  175  
 Arg Lys Glu Ser Glu Leu Ile Leu Thr Asn Leu Cys Phe Ala Phe Phe  
                   180                  185                  190  
 Asn Thr Asn Ala Tyr Ala Lys  
                   195

&lt;210&gt; 195

&lt;211&gt; 2874

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

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&lt;210&gt; 196

&lt;211&gt; 609

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

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 20 25 30  
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 35 40 45  
 Ala Ser Gly Lys Pro Leu Gly Glu Ile Ser Val Pro Leu Asp Ser Ser  
 50 55 60  
 Leu Leu Cys Thr Leu Ser Ser Glu Ser His Gln Glu Ala Ala Ser Asn  
 65 70 75 80  
 Glu Asn Asp Lys Lys Pro Gly Asn Tyr Lys Ser Met Leu Arg Pro Glu  
 85 90 95  
 Val Gly Thr Thr Ser Gln Asp Ser Ala Leu Leu Asp Gln Glu Leu Tyr  
 100 105 110  
 Asn Ser Phe His Phe Trp Arg Thr Pro Leu Pro Glu Ile Asp Leu Asp

115	120	125
Ile Glu Leu Glu Gln Asn Ser Gly Gly Lys Pro Ser Pro Glu Gly Pro 130 135 140		
Glu Glu Glu Ser Glu Gly Pro Val Pro Ser Ser Pro Asn Ile Thr Met 145 150 155 160		
Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu Asn Leu Glu Pro His 165 170 175		
Ile Asp Asp Pro Asp Val Lys Ala Gln Val Glu Val Leu Ser Ala Ala 180 185 190		
Leu Arg Ala Ser Ser Leu Asp Ala His Glu Glu Thr Ile Ser Ile Glu 195 200 205		
Lys Arg Ser Asp Leu Gln Asp Glu Leu Asp Ile Asn Glu Leu Pro Asn 210 215 220		
Cys Lys Ile Asn Gln Glu Asp Ser Val Pro Leu Ile Ser Asp Ala Val 225 230 235 240		
Glu Asn Met Asp Ser Thr Leu His Tyr Ile His Ser Asp Ser Asp Leu 245 250 255		
Ser Asn Asn Ser Ser Phe Ser Pro Asp Glu Glu Arg Arg Thr Lys Val 260 265 270		
Gln Asp Val Val Pro Gln Ala Leu Leu Asp Gln Tyr Leu Ser Met Thr 275 280 285		
Asp Pro Ser Arg Ala Gln Thr Val Asp Thr Glu Ile Ala Lys His Cys 290 295 300		
Ala Tyr Ser Leu Pro Gly Val Ala Leu Thr Leu Gly Arg Gln Asn Trp 305 310 315 320		
His Cys Leu Arg Glu Thr Tyr Glu Thr Leu Ala Ser Asp Met Gln Trp 325 330 335		
Lys Val Arg Arg Thr Leu Ala Phe Ser Ile His Glu Leu Ala Val Ile 340 345 350		
Leu Gly Asp Gln Leu Thr Ala Ala Asp Leu Val Pro Ile Phe Asn Gly 355 360 365		
Phe Leu Lys Asp Leu Asp Glu Val Arg Ile Gly Val Leu Lys His Leu 370 375 380		
His Asp Phe Leu Lys Leu Leu His Ile Asp Lys Arg Arg Glu Tyr Leu 385 390 395 400		
Tyr Gln Leu Gln Glu Phe Leu Val Thr Asp Asn Ser Arg Asn Trp Arg 405 410 415		
Phe Arg Ala Glu Leu Ala Glu Gln Leu Ile Leu Leu Leu Glu Leu Tyr 420 425 430		
Ser Pro Arg Asp Val Tyr Asp Tyr Leu Arg Pro Ile Ala Leu Asn Leu		



435                      440                      445  
 Cys Ala Asp Lys Val Ser Ser Val Arg Trp Ile Ser Tyr Lys Leu Val  
 450                      455                      460  
 Ser Glu Met Val Lys Lys Leu His Ala Ala Thr Pro Pro Thr Phe Gly  
 465                      470                      475                      480  
 Val Asp Leu Ile Asn Glu Leu Val Glu Asn Phe Gly Arg Cys Pro Lys  
 485                      490                      495  
 Trp Ser Gly Arg Gln Ala Phe Val Phe Val Cys Gln Thr Val Ile Glu  
 500                      505                      510  
 Asp Asp Cys Leu Pro Met Asp Gln Phe Ala Val His Leu Met Pro His  
 515                      520                      525  
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 530                      535                      540  
 Ala Lys Thr Leu Arg Gln Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala  
 545                      550                      555                      560  
 Phe Ala Ser Cys His Gln Glu Ala Val Glu Gln Thr Ile Met Ala Leu  
 565                      570                      575  
 Gln Met Asp Arg Asp Ser Asp Val Lys Tyr Phe Ala Ser Ile His Pro  
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 Ala Ser Thr Lys Ile Ser Glu Asp Ala Met Ser Thr Ala Ser Ser Thr  
 595                      600                      605

Tyr

<210> 197  
 <211> 2029  
 <212> DNA  
 <213> Homo sapiens

<400> 197  
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&lt;210&gt; 198

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 198

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Met Glu Gln Trp Glu Arg Leu Phe Glu Met Gly Phe Ala Ser Phe Cys
  1             5             10            15

Asn Ile Met Ile Ser Leu Val Pro Tyr Ser Tyr Leu Met Leu Ala Leu
      20             25             30

Thr Tyr Pro Gln Glu Ala Asp Thr Glu Val Ser Leu Arg Arg Gly Asp
      35             40             45

Ile Trp Val Met Phe Glu His Ala Gly Ala Met Gly Ser Leu Val Ser
      50             55             60

Asp Gly Gly Glu Gly Thr Arg Trp His Leu Leu Ala Glu Ala Asn Arg
      65             70             75             80

Asn Cys Thr Ser Pro Leu
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&lt;210&gt; 199

&lt;211&gt; 2304

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 199

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ggctctgagt tcttgtcccc tgtctaggaa gaatgaggtt atgcagacaa ctgggtgaac 660
aaggcaggca ggagctttat tgagtgcagc aacagctgtc aggagacca aagtgggtag 720

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aaaaaaaaa aaaaaaaaaa aaaa 2304

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&lt;210&gt; 200

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 200

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Met Ala Gln Gly Ala Pro Arg Ser Gly Leu Pro Glu Gly Leu Gln Leu
 1             5             10             15

Phe Ser Thr Ser Cys Tyr Leu Gln Cys Gly Glu Trp Gly Asp Met Phe
      20             25             30

Gln Pro Ile Cys Val Thr Ala Leu Ser Val Pro Pro Pro Cys Ser Gly
      35             40             45

Pro Trp Leu Met Gly Trp Thr Ser Pro Thr Ala Ala Ser His His Val
      50             55             60

Gly Trp Pro Leu Ser Thr Ser Arg Gly Trp Glu Gly Tyr Ser Val Asn
      65             70             75             80

Ser Ser Ser Ser Ser Glu Val Trp Ala Pro Arg Arg Val Ala Ile Leu
      85             90             95

Tyr Ser His Ser Pro Gly Ala Cys His His Pro Gln Leu Ser Glu Leu
      100            105            110

Val Lys Asn Met Leu Gln Leu Leu Ser Leu Pro Pro Phe Ser Arg Ser
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&lt;210&gt; 201

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 <212> DNA  
 <213> Homo sapiens

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<210> 202  
 <211> 299  
 <212> PRT  
 <213> Homo sapiens

<400> 202  
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 Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala Gly  
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 Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val Pro  
 35 40 45  
 Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His  
 50 55 60  
 Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe  
 65 70 75 80  
 Val Gly Val Asn Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu  
 85 90 95  
 Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly

100 105 110  
 Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val  
 115 120 125  
 Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe Tyr  
 130 135 140  
 Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr Leu Val  
 145 150 155 160  
 Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro Val Leu  
 165 170 175  
 Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro Glu Thr  
 180 185 190  
 Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys Gly  
 195 200 205  
 Gly Pro Leu Trp Glu Ala Arg Asp Gln Glu Gln Asp Ser Leu Arg Pro  
 210 215 220  
 Gly Pro Ala Arg Gln Gln Thr Gly Ala Pro Ala Pro Ser Ser Lys Lys  
 225 230 235 240  
 Arg Leu Ser Ala Ser Leu Ile Thr Ala Ser Lys Thr Arg Ala Pro Gln  
 245 250 255  
 Pro Leu Gly Pro Pro Gly Ala Met Gly Cys Arg Gly Leu Leu Cys Arg  
 260 265 270  
 Leu Met Leu Gln Ala Ala Glu Gly Thr Gly Gly Phe Ala Leu Leu Leu  
 275 280 285  
 Thr Ala Val Arg Pro Arg Arg Pro Ser Leu His  
 290 295

&lt;210&gt; 203

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 203

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 ccatttgagc tgtgatctga aggaacacta gtaagtagtc agctaggcac agatggggag 180  
 aggagagggc attctgggcc gaggacacag cgtgggtgaa atcctggagg tgggaagcgg 240  
 cactgtgctc cagagggact ggaggagagc cagagtgcact ggcacatcag gagggcacag 300  
 gggatgcccg agctgctggt gagacagaca ggactgagag aaacagcaag ctggtctctg 360  
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 ctgttttccc cagtgccttt tctttccttt ccctgttctt ccttttgaa gaacatacga 480  
 gctcacctgt gttctgggtc cttttctaaa gggctttatg attacttaac caacctcata 540  
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 tcgtttcaca gaagtggaaa ctgggggtgca gaaagatgaa gggtcagcag ctggtcagtg 660  
 acgagccagg gtccaaggcc aggatgtctg ccagccgcc atgctcactg cctttcatct 720  
 tggttctcct aggaagagtt agttacttct agggattat tagattggtg caaaagtaat 780  
 tgtggggttt gccattgaaa ataattactt ctacaccaac ctaatacttt ttcccagg 840  
 ggttagtag aaggattcct gcagaccaga aaccagagg gatattgctg atgtggtagg 900

tggtgggcca gcagggagag aggtctgagc cctgccagg tgctacctgg gagccacttt 960  
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<210> 204

<211> 111

<212> PRT

<213> Homo sapiens

<400> 204

Met Pro Glu Leu Leu Val Arg Gln Thr Gly Leu Arg Glu Thr Ala Ser  
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Trp Ser Leu Thr Ala Ser Arg Gln Val Val Ile Cys Leu Pro Ser Ser  
 20 25 30

Ser Pro Ala Leu Pro Leu Ser Leu Phe Ser Pro Val Pro Phe Leu Ser  
 35 40 45

Phe Pro Cys Ser Ser Phe Trp Lys Asn Ile Arg Ala His Leu Cys Ser  
 50 55 60

Gly Ser Phe Ser Lys Gly Leu Tyr Asp Tyr Leu Thr Asn Leu Ile Thr  
 65 70 75 80

Met Asp Gln Pro Thr Phe His Lys Tyr Ser Leu Lys Thr Ser Leu Leu  
 85 90 95

Leu Ser Pro Ser Phe His Arg Ser Gly Asn Trp Gly Ala Glu Arg  
 100 105 110

<210> 205

<211> 1395

<212> DNA

<213> Homo sapiens

<400> 205

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 tcgcttgaac ccaggaggca gaggttgcag tgagctgaga ttgtgctatt gcactccagc 180  
 ctggataaca agagcgagac tccgtctcaa aaaaaaaaaa aaattttagt agatagtgtt 240  
 ttgctacgtt actcagggtg gtctcaaact cctggcctca ggcagttctg cctaggcttc 300  
 ccaaagtact gggattacag gcagaagcca ctgcgcctac catagaatat tagttatctt 360  
 ttgaagtgat taaaaaggga aaagattttt ttccaagttt aatgatgaga aaagtgaag 420  
 aacagttatt ttaaagcccc tgatatttcc aacatctagg tcataaatga gtctcgttct 480  
 gttgatagct ttatctcttg gtaatgtgca tgctgtgtg tgtgtgtgtg tgtgtgttct 540  
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 gagactgagg tagatggtat tctgtgtctg gatataggca cgcctctccc atcaggccaa 660  
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aacccaaaaa actgtcaagg tcatcaggaa caaaacatag ccaatagcca agaaactgtc 1320  
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 aaaaaaaaaa aaaaa 1395

<210> 206  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Met Ala Asn Ile Met Tyr Thr Arg Pro Val Glu Thr Glu Val Asp Gly  
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 Ile Leu Cys Leu Asp Ile Gly Thr Pro Leu Pro Ser Gly Gln Leu Pro  
 20 25 30  
 Val Thr Leu Ser Gln Pro Ser Leu Glu Leu Arg Trp Ile Trp Ile Leu  
 35 40 45  
 Met Leu Val Ser Leu Cys Ser Val Tyr Leu Gly Cys Cys Tyr Leu Val  
 50 55 60  
 Pro Gly Ala Trp Gly Thr Arg Trp Phe Phe Phe Ser Val Ser Val Pro  
 65 70 75 80  
 Leu Leu Ala Phe Leu Ser Pro Ile Met Pro Pro Ser Gln Arg Gly Ser  
 85 90 95  
 Leu Tyr Ser Tyr Pro Cys Pro Phe Thr Ser Gly  
 100 105

<210> 207  
 <211> 1617  
 <212> DNA  
 <213> Homo sapiens

<400> 207  
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 tctgtcacca ttcaacctcc cactggagag ccctgttggt gaaatgattc tactcggaca 180  
 gaggaagtgc aggatgacaa ctgggggagag accaccacgg ccatcacagg cacctcggag 240  
 cacagcatat cccaagagga cattgccagg atcagcaagg acatggagga cagcgtgggg 300  
 ctggattgca aacgctacct gggcctcacc gtcgctctt ttcttggact tctagttttc 360  
 ctcaccccta ttgccttcat ccttttacct ccgatcctgt ggagggatga gctggagcct 420  
 tgtggcacia tttgtgaggg gctctttatc tccatggcat tcaaactcct cattctgctc 480  
 atagggacct gggcactttt ttccgcaag cggagagctg acatgccacg ggtgtttgtg 540  
 tttcgtgcc tttgttggt cctcattttt ctctttgtgg ttctctattg gcttttttac 600  
 ggggtccgca ttttggaactc tcgggaccgg aattaccagg gcattgtgca atatgcagtc 660  
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 tccccggcca tgattgctgc agctgctcgg cgcagggact caagccacaa cgagttgtat 1020  
 tatgaagagg ccgaacatga acggcgagta aagaagcggg aagcaaggct ggtggttgca 1080  
 gtggaagagg cctcatcca cattcagcgt ctccaggctg aggagcagca gaaagcccca 1140  
 ggggaggtga tggaccctag ggaggcggc caggccattt tccctccat ggccagggtc 1200  
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 tgcttgact tcagcctcgt agtcaatgtg aagaaaattc cattcatcat actctctgaa 1500  
 gagttcatag accccaaatc tcacaaattt gtccttcgct tacagtctga gacatccgtt 1560  
 taaaagttct atatttgtgg ctttattaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1617

<210> 208

<211> 426

<212> PRT

<213> Homo sapiens

<400> 208

Met Glu Asp Ser Val Gly Leu Asp Cys Lys Arg Tyr Leu Gly Leu Thr  
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Val Ala Ser Phe Leu Gly Leu Leu Val Phe Leu Thr Pro Ile Ala Phe  
 20 25 30

Ile Leu Leu Pro Pro Ile Leu Trp Arg Asp Glu Leu Glu Pro Cys Gly  
 35 40 45

Thr Ile Cys Glu Gly Leu Phe Ile Ser Met Ala Phe Lys Leu Leu Ile  
 50 55 60

Leu Leu Ile Gly Thr Trp Ala Leu Phe Phe Arg Lys Arg Arg Ala Asp  
 65 70 75 80

Met Pro Arg Val Phe Val Phe Arg Ala Leu Leu Leu Val Leu Ile Phe  
 85 90 95

Leu Phe Val Val Ser Tyr Trp Leu Phe Tyr Gly Val Arg Ile Leu Asp  
 100 105 110

Ser Arg Asp Arg Asn Tyr Gln Gly Ile Val Gln Tyr Ala Val Ser Leu  
 115 120 125

Val Asp Ala Leu Leu Phe Ile His Tyr Leu Ala Ile Val Leu Leu Glu  
 130 135 140

Leu Arg Gln Leu Gln Pro Met Phe Thr Leu Gln Val Val Arg Ser Thr  
 145 150 155 160

Asp Gly Glu Ser Arg Phe Tyr Ser Leu Gly His Leu Ser Ile Gln Arg  
 165 170 175

Ala Ala Leu Val Val Leu Glu Asn Tyr Tyr Lys Asp Phe Thr Ile Tyr  
 180 185 190

Asn Pro Asn Leu Leu Thr Ala Ser Lys Phe Arg Ala Ala Lys His Met  
 195 200 205

Ala Gly Leu Lys Val Tyr Asn Val Asp Gly Pro Ser Asn Asn Ala Thr  
 210 215 220

Gly Gln Ser Arg Ala Met Ile Ala Ala Ala Arg Arg Arg Asp Ser  
 225 230 235 240

Ser His Asn Glu Leu Tyr Tyr Glu Glu Ala Glu His Glu Arg Arg Val  
 245 250 255



Lys Lys Arg Lys Ala Arg Leu Val Val Ala Val Glu Glu Ala Phe Ile  
 260 265 270  
 His Ile Gln Arg Leu Gln Ala Glu Glu Gln Gln Lys Ala Pro Gly Glu  
 275 280 285  
 Val Met Asp Pro Arg Glu Ala Ala Gln Ala Ile Phe Pro Ser Met Ala  
 290 295 300  
 Arg Ala Leu Gln Lys Tyr Leu Arg Ile Thr Arg Gln Gln Asn Tyr His  
 305 310 315 320  
 Ser Met Glu Ser Ile Leu Gln His Leu Ala Phe Cys Ile Thr Asn Gly  
 325 330 335  
 Met Thr Pro Lys Ala Phe Leu Glu Arg Tyr Leu Ser Ala Gly Pro Thr  
 340 345 350  
 Leu Gln Tyr Asp Lys Asp Arg Trp Leu Ser Thr Gln Trp Arg Leu Val  
 355 360 365  
 Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val  
 370 375 380  
 Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro  
 385 390 395 400  
 Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe  
 405 410 415  
 Val Leu Arg Leu Gln Ser Glu Thr Ser Val  
 420 425

<210> 209  
 <211> 2259  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (2194)

<400> 209  
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tcctccccgg gctcctggga gccccgggc cctcaatccc caggactatg tggccacggg 1140
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<210> 210

<211> 327

<212> PRT

<213> Homo sapiens

<400> 210

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Met Met Phe Leu Ile Ser Pro Gly Ala Ala Gly Gly Ser Leu Leu Leu
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Met Gly Leu Leu Ala Ala Leu Leu Thr Ala Arg Gly Gly Pro Ser Ser
      20               25              30

Trp Gly Tyr Val Ser Gln Ala Leu Leu Phe His Gln Val Arg Lys Tyr
      35               40              45

Leu Leu Arg Leu Asp Val Arg Lys Asp His Val Lys Phe Trp Arg Pro
      50               55              60

Gln Leu Leu Leu Leu Val Gly Asn Pro Arg Gly Ala Leu Pro Leu Leu
      65               70              75              80

Arg Leu Ala Asn Gln Leu Lys Lys Gly Gly Leu Tyr Val Leu Gly His
      85               90              95

Val Thr Leu Gly Asp Leu Asp Ser Leu Pro Ser Asp Pro Val Gln Pro
      100              105             110

Gln Tyr Gly Ala Trp Leu Ser Leu Val Asp Arg Ala Gln Val Lys Ala
      115              120             125

Phe Val Asp Leu Thr Leu Ser Pro Ser Val Arg Gln Gly Ala Gln His
      130              135             140

Leu Leu Arg Ile Ser Gly Leu Gly Gly Met Lys Pro Asn Thr Leu Val
      145              150             155             160

Leu Gly Phe Tyr Asp Asp Ala Pro Pro Gln Asp His Phe Leu Thr Asp

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165 170 175  
 Pro Ala Phe Ser Glu Pro Ala Asp Ser Thr Arg Glu Gly Ser Ser Pro  
 180 185 190  
 Ala Leu Ser Thr Leu Phe Pro Pro Pro Arg Ala Pro Gly Ser Pro Arg  
 195 200 205  
 Ala Leu Asn Pro Gln Asp Tyr Val Ala Thr Val Ala Asp Ala Leu Lys  
 210 215 220  
 Met Asn Lys Asn Val Val Leu Ala Arg Ala Ser Gly Ala Leu Pro Pro  
 225 230 235 240  
 Glu Arg Leu Ser Arg Gly Ser Gly Gly Thr Ser Gln Leu His His Val  
 245 250 255  
 Asp Val Trp Pro Ser Thr Cys Cys Gly Pro Gly Val Gly Pro Ala Met  
 260 265 270  
 Trp Met Ser Ala Ala Ser Ser Cys Cys Arg Trp Gln Pro Ser Trp Ala  
 275 280 285  
 Trp Cys Pro Leu Gly Ile Ala Pro Gly Ser Gly Ser Ser Cys Ala Trp  
 290 295 300  
 Gly Leu Gly Arg Arg Leu Gly Arg Pro Arg Ala Ala Ala Gly Thr Ala  
 305 310 315 320  
 Glu Pro Thr Glu Asp Pro Gly  
 325

&lt;210&gt; 211

&lt;211&gt; 1001

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (812)

&lt;400&gt; 211

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 agaccatcat agtgctccca tcaaattgca tcaactcttc ccaagcagag aaaccggaac 180  
 ccaccaacca ggggcaggat agcctgaaga aacatctaca cgcagaaatc aaagttattg 240  
 ggactatcca gatcttgtgt ggcattgatg tattgagctt ggggatcatt ttggcatctg 300  
 ctctctcttc tccaaatctt acccaagtga cttctacact gttgaactct gcttaccat 360  
 tcataggacc cttttttttt atcatctctg gctctctatc aatcgccaca gagaaaagg 420  
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<210> 212  
 <211> 242  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (239)

<400> 212

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Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
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Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
      20           25           30

Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
      35           40           45

Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
      50           55           60

Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
      65           70           75           80

Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
      85           90           95

Ile Ser Gly Ser Leu Ser Ile Ala Thr Glu Lys Arg Leu Thr Lys Leu
      100          105          110

Leu Val His Ser Ser Leu Val Gly Ser Ile Leu Ser Ala Leu Ser Ala
      115          120          125

Leu Val Gly Phe Ile Ile Leu Ser Val Lys Gln Ala Thr Leu Asn Pro
      130          135          140

Ala Ser Leu Gln Cys Glu Leu Asp Lys Asn Asn Ile Pro Thr Arg Ser
      145          150          155          160

Tyr Val Ser Tyr Phe Tyr His Asp Ser Leu Tyr Thr Thr Asp Cys Tyr
      165          170          175

Thr Ala Lys Ala Ser Leu Ala Gly Thr Leu Ser Leu Met Leu Ile Cys
      180          185          190

Thr Leu Leu Glu Phe Cys Leu Ala Val Leu Thr Ala Val Leu Arg Trp
      195          200          205

Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu Phe Leu Pro His
      210          215          220

Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met Thr His Xaa Leu
      225          230          235          240

Trp Ile

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<210> 213  
 <211> 1079  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
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 gttgacacag ccgtgactta caattaaacc ctttcaatta cagtacagat tctgtgtgct 180  
 acttgatgag atgttaccca aggccagttt ggacttactg cttttgtccc tcatattaaa 240  
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Ser Pro Ser Ser Cys Val Ala Phe Val Thr Ser Phe Leu Gln Gly Ser  
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Ser Pro Arg Phe Gly Leu Arg Gln Val His Ser Arg Tyr His Pro Thr  
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Phe Leu Ser Lys Glu Gln Ala Ser His Thr Tyr Asn Pro Phe Pro Thr  
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Glu Ala Gln Ala Leu Gly Gly Arg Gly Phe Gly  
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International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C07K 14/00, 14/435, C12N 5/16,</b> <b>15/12, 15/63</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 99/58642</b> <b>(43) International Publication Date:</b> 18 November 1999 (18.11.99)																																							
<b>(21) International Application Number:</b> PCT/US99/10843 <b>(22) International Filing Date:</b> 14 May 1999 (14.05.99)  <b>(30) Priority Data:</b> <table border="0"><tr><td>60/085,472</td><td>14 May 1998 (14.05.98)</td><td>US</td></tr><tr><td>60/096,824</td><td>17 August 1998 (17.08.98)</td><td>US</td></tr><tr><td>60/099,950</td><td>11 September 1998 (11.09.98)</td><td>US</td></tr><tr><td>60/099,843</td><td>11 September 1998 (11.09.98)</td><td>US</td></tr><tr><td>60/100,424</td><td>15 September 1998 (15.09.98)</td><td>US</td></tr><tr><td>60/102,329</td><td>29 September 1998 (29.09.98)</td><td>US</td></tr><tr><td>60/103,615</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr><tr><td>60/111,799</td><td>11 December 1998 (11.12.98)</td><td>US</td></tr><tr><td>60/112,159</td><td>14 December 1998 (14.12.98)</td><td>US</td></tr><tr><td>60/114,415</td><td>31 December 1998 (31.12.98)</td><td>US</td></tr><tr><td>09/248,059</td><td>10 February 1999 (10.02.99)</td><td>US</td></tr><tr><td>09/287,150</td><td>6 April 1999 (06.04.99)</td><td>US</td></tr><tr><td>09/311,021</td><td>13 May 1999 (13.05.99)</td><td>US</td></tr></table> <b>(71) Applicant:</b> GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).		60/085,472	14 May 1998 (14.05.98)	US	60/096,824	17 August 1998 (17.08.98)	US	60/099,950	11 September 1998 (11.09.98)	US	60/099,843	11 September 1998 (11.09.98)	US	60/100,424	15 September 1998 (15.09.98)	US	60/102,329	29 September 1998 (29.09.98)	US	60/103,615	9 October 1998 (09.10.98)	US	60/111,799	11 December 1998 (11.12.98)	US	60/112,159	14 December 1998 (14.12.98)	US	60/114,415	31 December 1998 (31.12.98)	US	09/248,059	10 February 1999 (10.02.99)	US	09/287,150	6 April 1999 (06.04.99)	US	09/311,021	13 May 1999 (13.05.99)	US	<b>(72) Inventors:</b> WONG, Gordon, G.; 239 Clark Road, Brookline, MA 02146 (US). CLARK, Hilary, F.; 146 Webster Avenue #2, Cambridge, MA 02141 (US). FECHTEL, Kim; 46 Marion Road, Arlington, MA 02174 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US).  <b>(74) Agent:</b> MANDRAGOURAS, Amy, E.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).  <b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>  <b>(88) Date of publication of the international search report:</b> 2 March 2000 (02.03.00)
60/085,472	14 May 1998 (14.05.98)	US																																							
60/096,824	17 August 1998 (17.08.98)	US																																							
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60/103,615	9 October 1998 (09.10.98)	US																																							
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09/311,021	13 May 1999 (13.05.99)	US																																							
<b>(54) Title:</b> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  <b>(57) Abstract</b>  Novel polynucleotides and the proteins encoded thereby are disclosed.																																									

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EE	Estonia						

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/10843

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07K 14/00, 14/435; C12N 5/16, 15/12,15/63

US CL :435/69.1, 320.1, 325; 530/350; 536/23. 5

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 320.1, 325; 530/350; 536/23. 5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN, GENBANK, EST, BIOSCIENCE, MEDLINE, CAPLUS, GENESEQ

search terms: secrete? protein?, yeast, combinator?, ya15-1

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - A	Database Genbank, Accession number AA665330, EST nt89a10.s1. 18 February 1998.	1-4, 7 ----- 5, 8

☐

Further documents are listed in the continuation of Box C.

☐

See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*E* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
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*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

19 JULY 1999

Date of mailing of the international search report

17 DEC 1999

Name and mailing address of the ISA/US  
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Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

MICHAEL PAK

Telephone No. (703) 308-1234

**INTERNATIONAL SEARCH REPORT**International application No.  
PCT/US99/10843**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 164-166  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:  
  
Part or the whole claims were missing due to missing page 548.
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-5, 7-8

Remark on Protest

☐  
☐

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/10843

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-5, 7-8, drawn to YA15-1 polynucleotide, a host cell, and a process for producing a protein.

Group II, claim(s) 6 and 9-11 drawn to drawn to YA15-1 polypeptide and pharmaceutical composition.

Group III-Group CCXII are each drawn to a single claim from claims 12-163 and 167-223 which are independent polynucleotides or polypeptides. Claims 164-166 were missing text due to the missing page 548 of the claims.

and it considers that the International Application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below:

The inventions listed as Groups I-CCXII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features because the product of claim 1 is anticipated by Genbank AA665330, 18 February 1998 and thus, does not share a special technical feature with any other group.

The products of inventions II-CCXII, do not share the same or corresponding special technical feature with Group I, because they are drawn to products having different structures, and each defines a separate invention over the art. In this case, the different inventions are structurally distinct polynucleotides which encode a structurally distinct protein which has no specific disclosed function. Only the polynucleotide of each group can be used to produce the specific protein of the same group.

Since Groups I-CCXII do not share a special technical feature, unity of invention is lacking.